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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                   GENERAL INFO
                                                                                                                                                                                                                                                                                                            US-08-815-469-4
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                              RESULT 1
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Sequence 7652, Ap
Sequence 5, Appli
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Sequence 2, Appli
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                                                                           June 27, 2005, 13:37:17; Search time 44 Seconds (without alignments) 707.470 Million cell updates/sec
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Sequence 4, A
Sequence 4, A
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Sequence 3,
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1 MEQRPRGCAAVAAALLLVLL.....ERMGLDGCVEDLRSRLQRGP
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1: /cgn2_6/ptodatca1/iaa/5A_COMB.pep:*
 /cgn2_6/ptodatca1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodatca1/iaa/6A_COMB.pep:*
 /cgn2_6/ptodatca1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodatca1/iaa/PCTUS_COMB.pep:*
 /cgn2_6/ptodatca1/iaa/PCTUS_COMB.pep:*
 /cgn2_6/ptodatca1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-153-927-2
US-09-153-927-2
US-08-928-069-10
US-08-828-683A-6
US-09-557-908-4
US-09-333-966-4
US-09-333-966-4
US-09-933-966-4
US-09-933-966-4
US-09-933-966-4
US-09-933-966-4
US-09-933-966-4
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US-09-957-908-2
US-09-957-908-2
US-09-957-908-2
US-08-928-069-1
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US-09-006-353A-3
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Maximum Match 100%
Listing first 45 summaries
                                                   - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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No.
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US-09-527-236A-5 US-08-654-970-2 US-09-55-918-4 US-09-573-966-3 US-09-573-968-3 US-09-525-656B-3 US-09-523-323-3 US-09-55-908-5 US-09-756-884-5 US-09-756-884-5 US-09-756-884-5 US-09-756-884-5 US-09-756-874-138-3 US-09-974-138-3 US-09-933-966-5 US-09-933-966-5 US-09-933-966-5 US-09-086-493A-5 US-09-086-493A-5 US-09-527-236A-24	US-09-756-854-24
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ALIGNMENTS

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Sequence Application US/08815469
Patent W. 61534024
GENERAL INFORMATION:
APPLICANT: Wi, Guo-Liang
APPLICANT: Ni, Guo-Liang
APPLICANT: Dixit, Viehva
APPLICANT: Genz, Reiner L.
APPLICANT: Genz, Reiner L.
APPLICANT: Dixit, Viehva
APPLICANT: Neachington
STATE: 1100 New York Ave., Nw, Suite 600
STATE: 120005-3934
COMPUTER READABLE FORM:
MCDIUM TYPE: PLOPPY disk
COMPUTER: TEM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/815,469
FILING DATE: HERBWITH
CLASSIFICATION NUMBER: US 60/013,285
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FRING APPLICATION NUMBER: US 60/013,285
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### Sequence 5, Application US/09565918

### Patent No. 6433147

### GENERAL INPORMATION:

### APPLICANT: Ni, Jian

### APPLICANT: Rosen, Craig A.

### APPLICANT: Pan, James G.

### APPLICANT: Dixit, Vishva M.

### TITLE OF INVENTION: Death Domain Containing Receptor 4

### FILE REFERENCE: 1488130000-05-05

### CURRENT APPLICATION NUMBER: US 60/132,922

### PRIOR PILING DATE: 1999-05-06

### PRIOR PILING DATE: 1999-01-27

### PRIOR PILING DATE: 1998-01-27

### PRIOR PILING DATE: 1998-01-27

### PRIOR PILING DATE: 1997-02-05

### PRIOR PILING DATE: 1
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Matches 417; Conservative
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ORGANISM: Homo sapiens
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Sequence 2, Application US/09153927A

Patent No. 6297022

GENERAL INFORMATION:

APPLICANT: McDonnell, Peter C.

APPLICANT: Young, Peter R.

TITLE OF INVENTION: A Method of Identifying Agonists and

TITLE OF INVENTION: and TRS

CURRENT APPLICATION NUMBER: US/09/153,927A

CURRENT FILING DATE: 1998-09-16

EARLIER APPLICATION NUMBER: 60/061,334

EARLIER FILING DATE: 1997-10-08

NUMBER OF SEQ ID NOS: 11

SEQ ID NOS: 11

SEQ ID NOS: 11

SEQ ID NOS: 11

SEQ ID NOS: 11
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                                                     100.0%; Score 2323; DB 3; Length 417; 100.0%; Pred. No. 1.1e-193;
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US-08-815-469-4
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                        DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                                   9
                                                                                                                                       61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG
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                                                                                                                 361 IEAVEVEIGRFRDOQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP
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                                                                                                                                                                                                                                                                        Sequence 6, Application US/08828683A

Patent No. 6469144

GENERAL INFORMATION—
APPLICANT ABhtenai, Avi J.

TITLE OF INVENTION—Apo-2 LI AND Apo-3 FOLYPEPTIDES
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS: 7

ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94080

COMPUTER READABLE FORM:
COMPUTER: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: WinPat: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 06/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: MARSEART ON NUMBER: 35,600
REFRENCE/DOCKEY NUMBER: 9100791
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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STATE: California
COUNTRY: USA
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TYPE: Amino Acid
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
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                                                                                                                                  361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
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100.0%; Pred. No. 1.1e-193;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                           US-08-928-069-10
Sequence 10, Application US/08928069
Sequence 10, Application US/08928069
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
MUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
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FILING DATE: 09/23/1996
ATTORNEY/AGENT INPORMATION:
NAME: MATSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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Amino Acid
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Best Local Similarity
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61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                                                                   361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                          361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGF 417
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                                                                                                                                                                                                                                                                         Sequence 5, Application US/09874138
Fatent No. 6743625
GENERAL INPORMATION:
APPLICANT: No. Jian
APPLICANT: No. Jian
APPLICANT: No. Jian
APPLICANT: No. Jian
APPLICANT: No. Guo-liang
APPLICANT: Rosen, Craig A.
TITLE REFERENCE: 1488.1310006
CURRENT APPLICATION NUMBER: US/09/874,138
CURRENT FILING DATE: 2001-06.06
FRIOR PRILING DATE: 2001-06.06
FRIOR PELING DATE: 1999-08-13
FRIOR PELING DATE: 1999-06-07
FRIOR PELING DATE: 1999-06-07
FRIOR PELING DATE: 1999-06-07
FRIOR APPLICATION NUMBER: 60/132,498
FRIOR FILING DATE: 1999-05-07
FRIOR APPLICATION NUMBER: 60/132,498
FRIOR PELING DATE: 1999-03-17
FRIOR APPLICATION NUMBER: 60/040,846
FRIOR FILING DATE: 1999-03-17
FRIOR PELING DATE: 1999-03-17
FRIOR FILING DATE: 1999-03-17
FRIOR FILING DATE: 1997-03-17
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Matches 417; Conservative
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ORGANISM: Homo sapiens
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                                                           DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                                                                                                                                                                CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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                             MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
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APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Oillon, Patrick J.
TITLE OF INVENTION Patrick J.
TITLE OF INVENTION Death Domain Containing Receptors
FILE REFERENCE: 1488.0310008
CURRENT FILING DATE: 1090-04-21
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1997-02-01
PRIOR FILING DATE: 1997-02-06
PRIOR PLING DATE: 1997-02-06
PRIOR PLING DATE: 1996-01-17
PRIOR PLING DATE: 1996-10-17
PRIOR PLING DATE: 1996-10-17
PRIOR FILING DATE: 1996-10-17
PRIOR FILING DATE: 1996-10-17
PRIOR PLING DATE: 1996-03-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09557908
Patent No. 6713061
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ORGANISM: Homo sapiens
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SEQ ID NO 4
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181 TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG
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417; Conservative
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US-09-949-016-7652
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Best Local Si
Matches 417;
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361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
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                                                                                                                               GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Obixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: No. 6759513 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTONNEY/AGENT INFORMATION:
ANNUMBER: MS 60/013,285
FILING DATE: 12-MAR-1996
ATTONNEY/AGENT INFORMATION:
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                                                            RESULT 8
US-09-333-966-4
'S Sequence 4, Application US/09333966
'Patent No. 6759513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REPERENCE/DOCKET NUMBER: 148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTESEQ for Windows Version 4.0

LENGTH: 446
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181 TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG
                                                                                                          241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW
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301 DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
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                                                                                                                                            361 IEAVEVEIGRPRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                             361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pan, James G.
APPLICANT: Pan, James G.
APPLICANT: Pan, James G.
APPLICANT: Bentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L) NUMBER OF SEGUENCES:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPOTER: IBM PC COMPAILED
COMPOTER: IBM PC COMPAILED
COMPOTER: PACHAIN PC-DOS/MS-DOS
SOFTWARE: PACHAIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448,868
FILING DATE: HEREWITH
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/013,895
FILING DATE: 27-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEPFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300004
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECHOME: (202) 371-2600
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100.0%; Pred. No. 2.7e-193;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: HUMAN GENOME SCIENCES, INC.: 9410 KEY WEST AVENUE
ROCKVILLE
                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09448868
Patent No. 6461823
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 833 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
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amino acid
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417; Conserval
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                                                                                                                                                                                                                                                                                                                  US-09-448-868-5
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Best Local S
Matches 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
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                                                                                                                       Sequence 5, Application US/09013895A
| Patent No. 6442363
| CENERAL INFORMATION:
| APPLICANT: Nosen, Craig A. |
| APPLICANT: Rosen, Craig A. |
| APPLICANT: Rosen, Carage G. |
| APPLICANT: Dixit, Vishva M. |
| TITLE OF INVENTION: Beath Domain Containing Receptor 4 (DR4: Death TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L) |
| TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L) |
| CORRESPONDENCE ADDRESS: 12 |
| CORRESPONDENCE ADDRESS: 14 |
| CORRESPONDENCE ADDRESS: 15 |
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,895A
FILING DATE: 27-JAN-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 2323; DB 3;
100.0%; Pred. No. 2.7e-193;
ive 0; Mismatches 0;
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NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300002
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2600
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 5:
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 417; Conservative
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MOLECULE TYPE: protein
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                                                                                               US-09-013-895A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                        236
                                                                                                                                                                                                                                                                                                188 VSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRG 416
                                                                                                                                   68 LKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCG 127
                                                                                                                                                                                                                                                                                                                                                               DEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQV 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TWSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGL 356
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                                     8 EAPRĞQLRGESAAPVPQALILIVILGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHY
                                                                                           LKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCG
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    QRPRG-----CAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKK1GLFCCRGCPAGHY
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US-19-257-908-2

Bequence 2, Application US/09557908

Patent No. 6713061

GENERAL INFORMATION:

APPLICANT: Wi, Jian

APPLICANT: Dillon, Patrick J.

APPLICANT: Dillon, Patrick J.

TITLE OF INVENTION: Death Domain Containing Receptors

FILE REFERENCE: 1488.0310008

CURRENT FILING DATE: 2000-04-21

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-06-28

PRIOR FILING DATE: 1997-03-11

PRIOR FILING DATE: 1997-03-11

PRIOR FILING DATE: 1997-03-11

PRIOR FILING DATE: 1997-02-06

PRIOR FILING DATE: 1996-0-20

PRIOR FILING DATE: 1996-0-17

PRIOR FILING DATE: 1996-0-17
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Pred. No. 8.6e-189;
1; Mismatches 5;
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97.1%;
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Best Local Similarity 97.19
Matches 409; Conservative
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ORGANISM: Homo sapiens
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TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
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                                                                                                                  DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                                                                         MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
                                                                                                                                                                                                                                                                      361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08815469
| Sequence 2, Application US/08815469
| Patent No. 6153402
| GENERAL INFORMATION:
| APPLICANT: Yu, Guo-Liang
| APPLICANT: Dixit, Vishva
| APPLICANT: Dixit, Vishva
| APPLICANT: Dixit, Vishva
| APPLICANT: Dixit, Nishva
| APPLICANT: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSPICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/815,469

FILING DATE: HEREWITH
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REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 amino acids
amino acid
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Matches 409; Conservative
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36,688
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STATE: California
COUNTRY: USA
                                                             TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acids
TOPOLOGY: linear
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Best Local Similarity 97.1
Matches 409; Conservative
                                                                                                                                                           MOLECULE TYPE: protein US-09-333-966-2
     REGISTRATION NUMBER:
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US-08-928-069-1
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                                                LKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCG
128 CKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYBHGDGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C. STREET: 1100 New York Ave., NW, Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishavia
APPLICANT: Ediner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Pox, P.L.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEACHILIS PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/33,966
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
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APPLICATION NUMBER: No. 6759513 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA: 06-FEB-1997
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-CT-1996
PRIOR APPLICATION DATA: US 60/013,285
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
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Patent No. 6759513
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGC
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                                                                                                                                                                                                                                                                                                                                      Indels
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REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                    97.6%; Score 2267; DB 4;
97.1%; Pred. No. 8.6e-189;
tive 1; Mismatches 5;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                         Query Match 45.2%; Score 1051; DB 4; Length 181; Best Local Similarity 100.0%; Pred. No. 1.3e-83; Matches 181; Conservative 0; Mismatches 0; Indels 0
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996

ATTORNEY/AGENT INFORMATION:
NAME: MAISCHANG, DANGE: 35,600
REPERBUCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPRAN: 650/225-5416
TELEPRAN: 650/225-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids:
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-928-069-1
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Run on:

June 27, 2005, 13:37:13; Search time 19 Seconds (without alignments) 2111.705 Million cell updates/sec

US-10-081-280-6 2323 1 MEQRPRGCAAVAALLLVLL......ERMGLDGCVEDLRSRLQRGP 417 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	tumor necrosis fac	tumor necrosis fac		tumor necrosis fac	apoptosis-mediatin	apoptosis-mediatin	Fas antigen precur	FAS soluble protei	tumor necrosis fac	serine proteinase	gene G4R protein -	ypothetical prote	nerve growth facto	MEGF6 protein - ra	nerve growth facto	G2R protein - vari	gene ox40 protein	death receptor-6 -	subtilisin-like pr	heparan sulfate pr	protein T22A3.8 [i		laminin alpha chai	laminin beta-2 cha	notch homolog - se	B-cell activation	trophozoite surfac	fac	aminin alpha 5 ch
SUMMARIES	QI	JC4302 t	GQMST1 t					JC2395	137383 E	I54182 t				A26431 n	T13954 M									-		T31070 n			F	<u>r</u> 10053
	DB	7	т	-	-	~	7	~	~	~	~	~	~	7	7	-	7	0	~	н	~	~	7	~	-	7	~	7	-	7
	Length	461	454	461	455	335	327	324	314	435	1548	349	348	425	1574	427	349	272	651	915	3707	2823	2823	3102	1801	2531	277	667	416	3635
d	Query Match	17.9	17.4	17.0	16.1	8.6	8.4	7.5	7.2	7.1	7.0	7.0	6.9	6.9	6.8	6.7	6.7	9.9	9.9	9.9	6.4	6.4	6.4	6.4	6.3	6.3		6.3	6.3	6.2
	Score	415	404.5	394.5	374	199.5	196	175	168	166	163.5	162.5	159.5	158	158	155.5	154.5	153.5	153.5	153.5	149.5	148	148	148	147.5	•	146	146	145.5	145
	Result No.	1	8	e	4	Ŋ	9	7	۵	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

T2 protein - myxom	furin (EC 3.4.21.7	probable proprotei	perlecan precursor	hypothetical prote	Delta-4 protein -	furin (EC 3.4.21.7	OX40 antigen precu	B cell-associated	laminin gamma-1 ch	laminin gamma-1 ch	uromodulin precure	laminin beta-2 cha	CD27 antigen precu	hypothetical prote	laminin alpha-1 ch
GQVZML	A43434	B48225	A38096	T28811	JC7569	T43251	S12783	A46476	MMMSB2	MMHUB2	S52111	S53869	A46517	T27684	S18253
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326	1680	915	4391	1557	989	1299	271	305	1607	1609	642	1798	260	2219	3712
6.2	6.2	6.2	6.2	6.1	6.1	0.9	5.9	5.9	5.9	5. 9.	5.9	5.9	5.9	5.9	5.9
144.5	144.5	143.5	143.5	142	141.5	138.5	138	138	138	138	137.5	137.5	136.5	136.5	136.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

 RESULT 1 JC4302 Lumor necrosis factor receptor p55 precursor - pig C,5pecies: Sus scrofa domestica (domestic pig) C,5pecies: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004 C,Accession: JC4302; PC4093 R,Suter: B.; Pauli, U. Gene 163, 263-266, 1995	
A,Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor. A,Reference number: JC4302; MUD:96011645; PMID:7590278 A,Accession: JC4302 A,Accession: JC4302 A,Accession: JC4302 A,Accession: JC4302	
A;Modecule vype: mayna A;Residues: 1-461 «SUT> A;Cross-references: UNIPROT:P50555; GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g114175 A;Accession: PC4093 A;Molecule vype: protein	7.5
A.Residues: 1-7 <su2> A.Experimental source: kidney cell line 15 C.Genetics:</su2>	
A;Gene: tnfr C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homol C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor	ŏ,
F;1-29/Domain: Bignal sequence #status predicted <sig> F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <mat> F;44-194/Domain: extracellular cysteine rich #status predicted <ext></ext></mat></sig>	
F;44-82/Domain: NGF receptor repeat homology <no1> F;44-82/Domain: NGF receptor repeat homology <ngf> F;84-126/Domain: NGF receptor repeat homology <ngf> F;211-231/Domain: transembrane #status predicted <tmm> F;211-47/Domain: signal transduction #status predicted <sit> F;54,145,151/Binding site: carbohydrate (ABR) (covalent) #status predicted</sit></tmm></ngf></ngf></no1>	
Query Match 17.9%; Score 415; DB 2; Length 461; Best Local Similarity 30.5%; Pred. No. 1.5e-20; Matches 140; Conservative 44; Mismatches 201; Indels 74; Gaps 18;	
OY 11 VAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCT 62	
 Db 14 VLRALLVDVYPAGVHGLVLHPGDREKRESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCL 73	
 Qy 63 EPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWF 122	
 Db 74 GPGLDTDCRECDNGTFTASEN-HLTQCLSCSKCRSEMSQVEISPCTVDRDTVCGCRKN 130	
Qy 123 VECQVSQCVSSSPPYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPT 181	
Db 131 QYRKYWSETLFQCLNCSLCPNGTVQLPCLEKQDTIC-NCHSGFFLRDKECVSCVN 184	
 QY 182 STLGSCPERCAAVCGWRQMFWQVLLAGLVVPLLLGATLTYTYRHCWPH 230	
Db 185 CKNADCKNLCPATSETRNDFQDTGTTVLLPLVIFFGLCLAFFLFVGLACRYQRWKPKLYS 244	

231 ------KPLVTADEAGMEALTPPPATHLSPLD--SAHTLLAPPDSSEKICTV 274

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Nicontains: tumor necrosis factor binding protein 1 (TNP blocking factor)
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: Rattus norvegicus (Norway rat)
CiAccession: B36555
R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; Chare Call Biol. 9, 705-715, 1990
A,Fitle: Molecular cloning and expression of human and rat tumor necrosis factor recepton A;Reference number: A36555; MUID:91090841; PMID:1702293
          Comment: This protein is one of two distantly related receptors for both TNF-alpha (cac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: B36555
A; Molecule type: mRNA
A; Residues: 1-461 <HIM>
                                                                      A;Gene: TNFR-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P25118; GB:M60468; NID:9199825; PIDN:AAA39751.1; PID:9199826
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Wol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A;Reference number: A40254; MUID:91246168; PMID:1645445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-454 <GO2>
A; Residues: 1-454 <GO2>
A; Residues: 1-454 <GO2>
A; Residues: 1-54 <GO2>
A; Cross-references: GB M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R; Barrett, E.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Feldma Bur. J. Immunol. 21, 1649-1656, 1991
A; Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis A; Reference number: S16677; MUID:91285014; PMID:1647956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:L26349; NID:g430732; PIDN:AAA59361.1; PID:g430733
R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
Mol. Immunol. 30, 165-176, 1993
A;Title: Genomic organization and promoter function of the murine tumor necrosis factor
A;Reference number: I57826; MUID:93156721; PMID:8381516
A;Accession: I57826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N'Alternate names: tumor necrosis factor receptor, 55K
C'Species: Mus musculus (house mouse)
C'Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
C'Accession: A38634; B40254; Šī6677; S19021; I54532; I57826
R'Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E
Proc. Natl. Acad. Sci. U.S.A. 89, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
A;Reference number: A38634; MUID:91187885; PMID:1849278
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                                                                                                                                                                     352
245 IICGKSTPVKEGEPEPLATAPSFG-----PITTFSPIPSFSPTTFSPVPSFSPISSP 297
                                                                                                                                                                                                                                                                       353 APAQLADADPATLYAVVDGVPPTRWKEFVRRLGLSEHEIERLELONGRCLREAOYSMLAE 412
                                                                                                        --ESPAG 323
                                                                                                                                                                                                                                     SPAMMLQPGP-QLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKR 381
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                                                                                                                                                                     298 TFTPCDWSNIKVTSPPKEIAPPPQGAG----PILPMPPASTPVPTPLPKWGGSAHSAHS
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A;Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
A;Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
F;Rothe, J.G.; Brockhaue, M.; Gentz, R.; Lesslauer, W.
Immunogenetics 34, 338-340, 1991
A;Title: Molecular cloning and expression of the mouse Inf receptor type A;Reference number: S19021; MUID:92039815; PMID:1657766
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A;Residues: 1-454 <ROT>
A;Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
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A;Cross-references: GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102
                                                                                                     275 QLVGNSWT---PGYPETQEALCPOVTWSWDQLPSRALGPAAAPTLSP---
                                                                                                                                                                                                                                                                                                                                                                  382 WRQ---QQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumor necrosis factor receptor 1 precursor - mouse
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A; Residues: 1-454 <RES>
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A; Residues: 1-454 < LEW>
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A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane proteir
F;1-29/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                        F;30-454/Product: tumor recrosis factor receptor type 1 #status predicted <MAT>
F;30-212/Domain: extracellular #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;44-82/Domain: NGF receptor repeat homology <NG3>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 DCPSPGRDIVCRECEKGTFTASQNYLR-QCLSCKTCRKEMSQVEISPCQADKDIVCGCK- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 GWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----ENQPQRYLSETHFQCVDCSPC--FNGTVTIPCKETQNTVCNCHAGFFLRESECVPC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SHCKKNEECMKLCLPPPLANVTNPQDSGTAVLLPLVILLGLCLLSFIFISLMCRY 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 RHCWP-----HKPLVTADEAGMEALTPPPATHLSPLDSAHTLL-----APPDSSEK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 SAHPQRPDNADLAI-----LYAVVDGVPPARWKEFWRFWGLSEHEIERLEMQNGRCLRE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 PISTLGSCP--ERCAAVC-----GWRQMFWVQVLLAGLVVPLLLGATLTYTY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 PRWRPEVYSIICRDPVPVKEEKAGKPLTPAPSPAFSPTSGFNPTLGFSTPGFSSPVSSTP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 ICTVQLVGNSW------TPGY-PETQEALC----PQVTWSWDQLPSRALGPAAAP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVETGR-FRD 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;213-235/Domain: transmembrane #status predicted <MEM>
F;236-454/Domain: intracellular #status predicted <INT>
F;54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 VAAALLLVLLGARAQGGT------RSPRCDCAGDFHKKIGLFCCRGCPAGHYLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

17.4%; Score 404.5; DB 1; Length
Best Local Similarity 27.2%; Pred. No. 7.5e-20;
Matches 127; Conservative 56; Mismatches 191; Indels
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tumor necrosis factor receptor 1 precursor - rat

A;Cross-references: UNIPROT:P22934; GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362 C;Comment: This protein is one of two known receptors for both TNR-alpha (cachectin) and C. Superfamily: tumor necrosis factor receptor type 1 (TNRR1); NGF receptor repeat homolog C;Keywords: duplication; glycoprotein; receptor; transmembrane protein F:1-29/Domain: signal sequence #status predicted <SIG>

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18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 N----QPQRYLSETHFQCVDCSPC--FNGTVTIPCKEKQNTVCNCHAGFFLSGNECTPC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 AGSPAMMLQPGP-QLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVGGR-FRDQQYEML 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCTEPCGNSTCLVCPQDTFLAWENHINSECARCQACDEQASQVALENCSAVADTRCGCKP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 PTSTLGSCP--ERCAAVC-----GWRQMFWVQVLLAGLVVPLLLGATLTYTYR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 ----SHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFIGLCLLFFICISLLCRYP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 H------CWPHKPLVTADEAGM--EALTPPPATHLSPLDSAHTLL-----APPD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 QWRPRVYSIICRDSAPVKEVEGEGIVTKPLTPASIPAFSPNPGFNPTLGFSTTPRFSHPV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 SSEKICTVQLVGNSWTPGYPETQEALCPQVTWSWDQLPSRALGPAAAPTLSP----ESP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 SSTPISPV-FGPSNWHNFVPPVREVV---PTQGADPLLYGSLNPVPIP--APVRKWEDVV 351
                                                                                                                                                                                                                                                                                                                                                                          11 VAAALLLVILGARAQG-----GTRSPR---CDCAGDFHKKIGLFCCRGCPAGHYLKA 59
                                                                                                                                                                                                                                                                                                                                                                                                                     11 LSLVLLALLMGIHPSGVTGLVPSLGDREKRDNLCPQGKYAHPKNNSICCTKCHKGTYLVS 70
F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted 330-211/Domain: extracellular #status predicted «EXT»
F;30-201/Product: tumor necrosis factor binding protein #status predicted F;44-82/Domain: NGF receptor repeat homology «NG1»
F;41-26/Domain: NGF receptor repeat homology «NG2»
F;127-167/Domain: NGF receptor repeat homology «NG3»
F;128-204/Domain: NGF receptor repeat homology «NG3»
                                                                                                                                                                     F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-461/Domain: intracellular #status predicted <INT>
F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                         73;
                                                                                                                                                                                                                                                                         DB 1; Length 461;
                                                                                                                                                                                                                                                                      17.0%; Score 394.5; DB 1; Length 27.9%; Pred. No. 3.6e-19; tive 55; Mismatches 202; Indels
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Best Local Similarity 27.9*
Matches 128; Conservative
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Unior necrosis factor receptor 1 precursor [validated] - human
N.Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N.Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein (;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A38208; A34899; A34990; A36555; C36555; A38281; S12057; JT0758; A60231; A38
R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A;Title: Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to che A;Reference number: A38208; MUID:92250049; PMID:131577

Accession: A34899

A;Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754 A;Experimental source: placenta A; Molecule type: mRNA A; Residues: 1-455 <LOE>

A; Molecule type: DNA
A; Residues: 1-455 cFUC.
A; Residues: 1-455 cFUC.
A; Residues: 1-455 cFUC.
A; Cross-references: UNIPROT: P19438; GB:M75864; GB:M75865; GB:M75866; NID: G339748; PIDN: A
Cross-references: UNIPROT: P19438; GB:M75864; GB:M75865; GB:M75866; NID: G339748; PIDN: A
R; Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lessalau
Cell 61, 351-359, 1990
A; Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor receptance number: A34899; MUID: 90235284; PMID: 2158862

A;Accession: A60594
A;Molecule type: protein
A;Residues: 41-43, "X, 45-53, "V', 55-57, "XK', 60 < 0LS>
A;Residues: 13 source: renal failure patient urine
B;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990

A;Note: part of this sequence, including the amino end of the mature protein, confirmed P R;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.; Cell 61, 361-370, 1990
A;Title: Molecular clonning and expression of a receptor for human tumor necrosis factor. A;Reference number: A34900; MUID:90235285; PMID:2158863 A; Molecule type: mRNA A; Residues: 1-455 <SCH> A; Cross-references: GB:M33294; NID:g339744; PIDN:AAA01210.1; PID:g339745 R; Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; C DNA Cell Biol. 9, 705-715, 1990 A; Title: Molecular cloning and expression of human and rat tumor necrosis factor recepton A; Reference number: A36555; MUID:91090841; PMID:1702293 Riseckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.

Eur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necroais factor inhibitor: purification, NH-2-terminal amino acid sequence
A;Reference number: A60231; MUID:90292116; PMID:2113477 A; Molecule type: mRNA
A; Residues: 1-455 kNDP>
A; Residues: 1-455 kNDP>
A; Residues: 1-655 kNDP>
A; Residues: 1-655 kNDP>
A; Reseronces: EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
A; Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, we R; Remper, O.; Wallach, D.
Gene 134, 209-216, 1993
A; Ritle: Cloning and partial characterization of the promoter for the human p55 tumor nec A; Reference number: JT0758; MUID:94085779; PMID:8262379
A; Reference number: JT0758; A Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: 30-38,141-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;107-128;162-167,'X',169-26
A; Note: the purified protein, called tumor necrosis factor binding protein, is a soluble
B; Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. (Natl. Acad. S21. U.S. A. 87, 7380-7384, 1990
Proc. (Natl. Acad. S21. U.S. A. 87, 7380-7384, 1990
A; Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of rec
A; Reference number: A38281; MUID:91017509; PMID:2170974 A; Molecule type: mRNA A; Residues: 1-455 cGRA> A; Cross-references: GBR37764 A; Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372 R; Nophar, Y: , Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann, BrBNO J. 9, 3269-3278, 1990 EMBO J. 9, 3269-3278, 1990 A;Modecule type: protein A;Residues: 41-43,'X',45-53,'X',55-57 <SEC> R;Gatenaga, T.; Hwang, C.; Kohr, W.; Cappuccini, P.; Lucci III, J.A.; Jeffes, E.W.B.; Ler Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990 A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto) A; Molecule type: protein
A; Residues: 41-60 <GAT>
A; Residues: 41-60 <GAT>
A; Residues: 41-60 <GAT>
A; Reperimental source: cancer patient serum
A; Rolsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
Bur. J. Haematol. 42, 270-275, 1989
A; Title: Isolation and characterization of a tumor necrosis factor binding protein from A; Reference number: A60594; MUID:89171156; PMID:2924890 A,Molecule type: mRNA A,Residues: 1-452 <HIM> A,Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756 A,Accession: C36555 le form of the receptor. A;Reference number: S12057; MUID:91006021; PMID:1698610 A;Accession: S12057 A;Reference number: A38258; MUID:91062364; PMID:2174164 A;Accession: A38258 A, Residues: 1-13 < KEM> A; Molecule type: DNA A; Accession: A38281 A;Accession: A36555

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A;Status: preliminary
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proteins purified from human urine. Evidence PMID:2153136
                                                                                             R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Blochem. S9, 2266, 2268, 1994
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified A;Reference number: JC2404; MUID:95128033; PMID:7765720
                                                                                                                                                                       A;Molecule type: protein
A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A;Experimental source: urine
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AAAPTLSP- 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 QKWEDSAHKPQSLDTDDPATLYAVVENVPLRWKEFVRRLGLSDHEIDRLELQNGRCLRE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 EC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TSTLGSCPE--RCAAVC-----GWRQMFWVQVLLAGLVVPLLLGATLTYTYRH 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---SNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 CWPHK-----PLVTADEAGMEALTPPPATHLSPLDS-----AHTLLAPPDSSEKIC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -WKSKLYSIVCGKSTPEKEGELEGTTTKP---LAPNPSFSPTPGFTPTLGFSPVPSSTFT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---ESPAGSPAMMLQPGP-QLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRD 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIELLVGIYPSGVIGLVPHLGDREKRDSVCPOGKYIHPQNNSICCTKCHKGTYLYNDCPG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.1%; Score 374; DB 1; Length 455; 28.3%; Pred. No. 8.2e-18; ative 49; Mismatches 183; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEAL 441
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   A, Title: Two tumor necrosis factor-binding A, Reference number: A35010; MUID:90110215;
                                                                               A; Experimental source: normal urine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 28.3%
Matches 131; Conservative
                                                  A, Molecule type: protein A, Residues: 41-45 < ENG>
                                 A, Accession: A35010
                                                                                                                                                            A; Accession: JC2404
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A,Accession: $24543
A,Status: preliminary
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Rosidues: 1-335 cKRA>
A,Cross-references: RMBL:X63717; NID:928741; PID:928742
A,Cross-references: RMBL:X63717; NID:928741; PID:928742
J. Biol. Chem. 267, 10709-10715, 1992
A,Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member c
A,Reference number: A38142; MUID:92268122; PMID:1375228
apoptosis-mediating surface antigen Fas precursor - human NyAlternate names: surface antigen APO-1 (5) Species: Homo sapiens (man) (5) Species: Homo sapiens (man) (5) Spate: 17-Jan-1992 #sequence revision 17-Jan-1992 #text_change 09-Jul-2004 (5) Date: 17-Jan-1992 #sequence revision 17-Jan-1992 #text_change 09-Jul-2004 (5) Accession: A40036; S24543; Ā38142 (A) Thirdhima, A: Yonehara, A: Yonehara, A: Mizushima, A:I:; Sameshima, M.; Hase, A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can media A: Reference number: A40036; MUID:91309137; PMID:1713127
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C; Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C; Keywords: apoptosis; surface antigen; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;85-128/Domain: NGF receptor repeat homology <NG4*>
F;174-190/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P25445; GB:M67454; NID:9182409; PIDN:AAA63174.1; PID:9182410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 TYRHCWPHKPLVTADBAGMEALTPPPATHLSPLDSAHTL---LAPPDSSEKICTVQLVGN 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----EHGI-IKECTLTSNTKCKEE----GSRSNLGWLCLLL-LPIPLIVWVKRKE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWTPGYPETQEALCPQVTWSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVM 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 VOKTCRKHR----KENQG-----SHESPTLNPETVAINLSDVDLSKYITTI----
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21.4%; Pred. No. 2.8e-06;
tive 43; Mismatches 106; IndelB 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BINCTRIQNIKCRCKENFF-----CNSTVCEHCDPCTKC-----
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A, Experimental source: SKM6.4 cells A, Note: sequence extracted from NCBI backbone (NCBIP:103810) A, Note: in NCBI backbone the source is designated as mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 DAVPARRWKEFVRTLGLREAEIEAVEVE-IGRFRDQQYEMLKRWRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Krammer, P.H. submitted to the EMBL Data Library, February 1992 A;Reference number: S24543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: GDB:APT1
A;Cross-references: GDB:132671; OMIM:134637
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Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-335 <ITO>
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A;Cross-treferences: DDB.1026113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g468489
A;Experimental source: liver
C;Genetics: C;Genetics: C;Aintrons: 62,1
C;Genetics: Carlor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: Lransmembrane protein
C;Keywords: Lransmembrane protein
F;1-21/Domain: signal sequence #status predicted <NGS-
F;1-21/Domain: NGF receptor repeat homology <NGF-
F;81-124/Domain: Lransmembrane #status predicted <TWM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 137383
R;Cascino, 1.; Fiucci, G.; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A;Tile: Three functional soluble forms of the human apoptosis-inducing Fas molecule
A;Reference number: 137383; MUID:95181785; PMID:7533181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 HYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 TCLPGFYEHGDGCVSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 ERKVKDCTTSGGAPTCHPCTEGEEYTDRKHYSDKCRRCAFCDEGHGLEVETNCTRTQNTK 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.2%; Score 168; DB 2; Length 314; Best Local Similarity 19.1%; Pred. No. 0.00034; Matches 66; Conservative 37; Mismatches 100; Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 BINCTRIQNTKCRCKPNFF-----CNSTVCEHCDPCTKC------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 7.5%; Score 175; DB 2; Local Similarity 28.5%; Pred. No. 0.00012; les 43; Conservative 17; Mismatches 67;
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A;Molecule type: mRNA
A;Residues: 1-314 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCKPGWFVECQVSQCVSSSPFYCQPCLDCG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRCKENFY -- CNASLC -- -- DHCYHCTSCG 146
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FAS soluble protein - human
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apoptosis-mediating membrane-associated polypeptide Fas - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46484; A47254
R;Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins, A;Title: The CDNA structure, expression, and chromosomal assignment of the mouse Fas ant A;Reference number: A46484; MUID:92148151; PMID:1371136
                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-37 < MAT:
A; Cross-references: UNIPROT: P25446; GB: M83649; NID: g193225; PIDN: AAA37593.1; PID: g193226
A; Experimental source: BAM3 macrophage cell line
A; Note: sequence extracted from NCBI backbone (NCBIN: 81544, NCBIP: 81545).
R; Adachi, M.; Wattanabe-Fukunaga, R.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A; Title: Aberrant transcription caused by the insertion of an early transposable element
A; Reference number: A47254; MUID: 93189576; PMID: 7680478
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A;Molecule type: mRNA
A;Residues: 1-374 <KIM>
A;Cross-references: UNIPROT:Q63199; DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d1005
A;Experimental source: thymus
A;Accession: PC2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506
A;Experimental source: MRL lpr/lpr
A;Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126863, Cs.Superfamaily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo C;Keywords: transmembrane protein
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NGF>
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: JC2395; PC2246
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated from of Fas antigen in the rat live
A;Reference number: JC2395; MUID:94128114; PMID:7507668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 ASCEHGILEPCTATSNINCRKQSPRNRLWLLTILV-LLIPLVF-IYRKYRKRKKWKRRQD 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- DCAGDFHKKIGLFCCRGCPAGHY
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8.4%; Score 196; DB 2; Length 327
Best Local Similarity 23.8%; Pred. No. 4.7e-06;
Matches 62; Conservative 25; Mismatches 109; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-96 <ADA>
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                                                                                                                                                                                                                                                                                                                                                    Status: preliminary
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C; Keywords: hydrolase; serine proteinase
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                                                  Query Match
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Matches
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R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Renomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequent A;Reference number: 154182; MUD:93252381; PMID:8486360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homold
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A,Cross-references: UNIPROT:Q04592; GB:D17583; NID:g407344; PIDN:BAA04507.1; PID:d100503
                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P36941; GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
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C.Species: Mus musculus (house mouse)
C.Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C.Accession: 834583
R.Nakagawa, T.; Murakami, K.; Nakayama, K.
PESB Lett. 137, 155-171, 1993
A;Title: Identification of an isoform with an extremely large Cys-rich region of 1
A;Reference number: 834583; MUID:93327934; PMID:8335106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---CLDCGALHRHTRLLCSRRDTDC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 GNSTCLVCPQDTFLAMENHHN--SECARCQACDEQASQVALENCSAVADTRCGCKPG--- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCLP-----GFYEHGDGCVSCPT---STLGSCPERCAAVCGWRQMFWVQVLLAGLVV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 --COPHTRCENOGLVEAAPGTAQSDTTCKNPLEPLPPEMSGT-------MLMLAVLL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 PLLLGATLTYTYRHCWPHKPLVTADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKIC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 PLAFFLLLATVFSCIWKSHPSL-CRKLGSLLKRRPQGEGPNP-------273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 TVQLVGNSWTP--GYPETQEALCPOVTWSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQ 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 ----VAGSWEPPKAHPYFPDLVQPLLPISGDVSPV-STGLPAAPVLEAGVPQQQSPLDLT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 LLLVLLGARAQG-----GTRSPRC-DCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPC 65
                                                                                                                            tumor necrosis factor receptor 2-related protein - human
C;Species: Homo sapiens (man)
C;Date: 24-May_1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.1%; Score 166; DB 2; Length 435; 11.1%; Pred. No. 0.00063; ve 43; Mismatches 153; Indels
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Best Local Similarity 21.1%;
Matches 77; Conservative 4
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A,Molecule type: mRNA
A,Residues: 1-1548 <NA
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A, Cross-references: UNIPROT: P34015, GB:X69198, NID:9456758; PIDN:CA449137.1; PID:9457087
A, Experimental source: strain India-1967, ssp. major, isolate Ind3
R;Kolykhalov, A.A.; Blinov, V.W.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolc submitted to the EMBL Data Library, April 1992
A, Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P (
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A;Experimental source: strain India-1967, isolate Ind3
A;Exbelvinov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A;Reference number: S32385; MUID:93202281; PMID:8384129
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                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      669 YNPHICSRCWSGYVIIPPNHTCQKLECRQGEFQDSE--YEEGMPCEEGCLGCTEDDPGAC 726
                                                                                                                                                                                                                                                                                                                                                                                                         616 OGSGPSNCTSCRADKHGQERFLYHGECLENCPVGHY-----PAKGHTCLPCPDNCELC 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- ARCQACDEQASQVALENCSAVADTRCGC--- KPGWF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 VECQVS-----QCVSSSP-----FYCQPC-LDCGALHRHTRLLCSRRDTDCGTCLPG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    727 ISCATGYYMFERHCYKACPEKTFGVKWECRACGTNCGSCDQH-------ECYWCEEG 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYEHGDGCV-SC----PISTLGSCPERCAAVC-----GWRQMFWVQVLLAGLVVPLLL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 GATLTYTYRHCWPHKPLVTADEAGMEALTPPPATHLSPLD------SAHTLLAPP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         831 GTCL-----WSTWPQVEGKDWNEAVPTEKPSLVRŚLLQDRRKWKVQIKRDATSQNQPC 883
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NiAlternate names: B2R protein (COP)
C;Species: variola virus
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: D36858; S46888; S32385; S35987
                                                                                                                                                                                                                                                                        25 QGGTRSPRCDCAGDFHKKIGLF----CCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLA
Length 1548;
       DB 2;
7.0%; Score 163.5; DB 2; ilarity 24.5%; Pred. No. 0.0031; Conservative 22; Mismatches 138;
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A;Experimental source: strain India-1967, ssp. major
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A;Accession: D36858
A;Status: preliminary
A;Molecule type: DNA
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A; Residues: 31-168 <SHC>
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                                                         Local Similarity
hes 82; Conserv
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A;Molecule type: DNA
A;Residues: 1-349 <KOL>
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A;Cross-references: GRIX61269
A;Cross-references: GRIX61269
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cs C;Comment: The cysteine-rich region of the extracellular domain may form part or all of t C;Comment: The systeine-rich region of the extracellular domain may form part or all of t C;Comment: This protein is thought to form a high-affinity receptor when it associates wi C;Genetics:
A;Introns: 20/3
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; tr
F;1-29/Domain: signal sequence #status predicted <SXI>F;10-25/Domain: signal sequence #status predicted <SXI>F;30-425/Product: nerve growth factor receptor #status predicted <MAT>F;30-6/Domain: NGF receptor repeat homology <NG3>F;31-6/Domain: NGF receptor repeat homology <NG3>F;10-148/Domain: nGF receptor repeat homology <NG3>F;10-14-145/Domain: nGF receptor repeat homology <NG4>F;10-145/Domain: nGF receptor re
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MEGF6 protein - rat
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
Cibate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
Cibate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
Cibate: 20-Sep-1999 #sequence_revision 20-Sep-1999
RiNakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs k
A;Reference number: Z14126; MUID:98360089; PMID:9693030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRCGCKPGWFVE------CQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 QPCGANQTVCEPCLDN---VTFSDVVSATE-----PCKPCTECLGLQSMSA--PCVEADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLPGFY - - - - EHGDGCVSCPT - - - - STLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 APC-----TEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEOASQVALENCSAVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 AVCRCAYGYYODEETGHCEACSVCEVGSGLVFSCQ--------DKQNTVCEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 LGATLTYTYRHCWPHKPLVTADEAGMBALTP-----PPATHLSPLDSAHTLLAPPDSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEQRPRGCAAV--AAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.8%; Score 158; DB 1; Length 425;
21.2%; Pred. No. 0.0021;
Ive 42; Mismatches 202; Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 llarity 21.2%;
Conservative 4
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Matches 102; Conserv
           A; Residues: 1-20 <MET>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein G2R - variola major virus C;Species: variola major virus C;Species: variola major virus C;Species: variola major virus C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004 C;Accession: T28653 R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin Nature 366, 748-751, 1993 A;Title: Potential virulence determinants in terminal regions of variola smallpox virus A;Reference number: Z20488; MUID:94088747; PMID:8264798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Meaidues: 1-425 - KAD.
A; Actoidues: 1-425 - KAD.
A; Cross-references: UNIPROT: P07174; GB: X05137; NID: 956755; PIDN: CAA28783.1; PID: 956756
R; Metsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
A; Metsis, M.; 247-254, 1992
A; Title: Regulatory elements and transcriptional regulation by testosterone and retinoic
A; Reference number: PH1229; MUID: 93077038; PMID: 1446821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: UNIPROT:P34015; EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g4391; Experimental source: strain Bangladesh 1975; Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nerved growth factor receptor precursor, low affinity - rat
N;Alternate names: NGF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A26431; PH1229
R;Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A;Reference number: A26431; MUID:87115859; PMID:3027580
                                                                                                                                                                                                                                                                                                                                        70 SGTFTS-RNNHLPACLSCNGRCN--SNQVETRSCNTTHNRICECSPGYY-----CLLK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 GSSGCKACVSQTKCGIGYGVSGHT---SVGDVICSPCGFGTYSHTVSSADKCEPVPNNT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QDTFLAWENHHNSECARCQA-CDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                  134 SPFYCQPCLD---CG---ALHRHTRLLCSRRDTDCGTCLPGFYEH----GDGCVSCPTST 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTFLAWENHHNSECARCQA-CDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSS 134
                                                                                                                                                     74
                                                                                                                                                                                                                 LSCIIINGRDAAPYTPPNGKCKDTEYKRHNL-CCLSCPPGTYASRLCDSKT-NTQCTPCG 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 PFYCQPCLD---CG---ALHRHTRLLCSRRDTDCGTCLPGFYEH----GDGCVSCPTST 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQ
                                                                                                                                                 LLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
7.0%; Score 162.5; DB 2; Length 349; 26.7%; Pred. No. 0.00087; live 21; Mismatches 84; Indels 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 348;
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26.8%; Pred. No. 0.0014;
7ative 20; Mismatches 84
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A;Molecule type: DNA
                                                                          Conservative
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Best Local Similarity
                                         Local Similarity
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A; Molecule type: DNA
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completed: June 27, 2005, 13:40:44
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Matches 104; Conservative
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Job time : 21 secs
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                                         A;Reaidues: 1-1574 «NRK»
A;Reaidues: 1-1574 «NRK»
A;Cross-references: UNIPROT:088281; EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF6
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A;Residues: 29-31, T., 33-42, TT', 45-46, TX', 50-51, XX', 54-56 <MAR>
A;Residues: 29-31, T., 33-42, TT', 45-46, TX', 50-51, XX', 54-56 <MAR>
A;Residues: 29-31, T., 33-42, TT' cell line A875
A;Note: this sequence has been corrected by a note added in proof to follow the nucleoting R;Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A;Title: Structural domains of the extracellular domain of human nerve growth factor rec A;Reference number: $21689; MUD:92198017; PMID:1372492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P08138; GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205 KR;Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman, G.; Thompson, S.; Grob, P.; J. Neurochem. 48, 225-232, 1987. A;A;Title: Purification and amino terminal sequencing of human melanoma nerve growth factors. A;Reference number: A60204; MUID:87085574; PMID:3025363
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A;Titlel: Expression and structure of the human NGF receptor.
A;Reference number: A25218; MUID:87051725; PMID:3022937
A;Accession: A25218
                                                                                                                                                                                                                                                                                                                                                                                                                                               990 CAQSCPPLTF-----GLNCSQICTCFNGAS-----CDSVTG-QCHCAPGWMGPTCLQ 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1089 COLNCSCLHGGICDRLTGHCLCPAGWTGDKCOSSCVSGTFGVHCEEHCACRKGASCHHVT 1148
                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1036 ACPPGLYGKNCQHS-CLCRNGGRCDPILGQCTCPEGWTGLACENE-----CLPGHYAAG 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1149 GACFCPPGWRGPHCEQACPRGWFGEACAQRCLCPINASC--HH--VTG-----ECRCPPG 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SCEQAC------QPGTFGKDCEHLCQCPGETWACD--PA 1234
                                                                                                                                                                                                                                                                                                                                                                                                   ----CPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWF----- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAGMEALTPPP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 ATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPG-YPETQEAL--CPQVTWSWDQLPS 305
                                                                                                                                                                                                                                                                                                                                               SGACTCPAGWR---GSFCEHACPAGFFGLDCDSACNCSAGAPCDAVTGSCICPAGRWGPR 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nerve growth factor receptor precursor, low affinity [validated] - human N'Alternate names: NGF receptor C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text_change 09-Jul-2004 C;Accession: A25218; A60204; $21689; IS7638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VECQVSQCVSSSPFYCQPCL-DCGALHRHTRLLCSRRDTDCGTCLPGFYE--
                                                                                                                                                                                                                                                                                                 30 SPRCDCAGDFHKKIGLFCCRGCPAGHY-----LKAPCTEPCGNSTCLV----
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                 6.8%; Score 158; DB 2; Length 1574;
24.5%; Pred. No. 0.0072;
.ive 16; Mismatches 120; Indels 142;
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                  Conservative
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A,Residues: 183-208 <VIS>
                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-427 <JOH>
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                         A;Molecule type: mRNA
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A Map position: 17q21-17q22

Cisuperfamily: nerve growth factor receptor; NGF receptor repeat homology
Cisuperfamily: nerve growth factor receptor; NGF receptor repeat homology
Cisuperfamily: nerve growth factor receptor; monomer; phosphoprotein; receptor; ti
Fi1-28/Domain: signal sequence #status predicted <SIG>
Fi29-250/Domain: extracellular #status predicted <SIG>
Fi29-250/Domain: extracellular #status predicted <EXT>
Fi32-65/Domain: NGF receptor repeat homology <NG3>
Fi09-147/Domain: NGF receptor repeat homology <NG3>
Fi199-147/Domain: NGF receptor repeat homology <NG3>
Fi191-248/Region: serine/threonine-rich
Fi29-27/Domain: transmembrane #status predicted <TRN>
Fi23-27/Domain: intracellular #status predicted <IRN>
Fi23-37/Domain: intracellular #status predicted <IRN>
Fi20/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                          A)Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma of
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of t
C;Comment: This protein is thought to form a high-affinity receptor when it associates wi
C;Comment: This receptor undergoes both N- and O-linked glycosylation.
Risehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
Alitle. A constitutive promoter directs expression of the nerve growth factor receptor of A; Reference number: 157638; MUID:89096903; PMID:2850481
A;Accession: 157638
A;Accession: is7638
A;Accession: breliminary; translated from GB/EMBL/DDBJ
A;Recule type: DNA
A;Residues: 1-22 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---VTFSDVVSATE-----PCKPCTEC-----VGLQSMSAPCVEADDAVCRCAYGYQD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------CQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFY----EH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 ETTGRCEACRVCEAGSGLVFSCQ------DKQNTVCEECPDGTYSDEANH 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 GDGCVSCPT----STLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 WPHKPLVTADEAGMEALTP--PPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGY 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 CSILAAVVVGLVAYIAFKRWNSCKQNKQGANSRPVNQTPPPPEGEKLHSDSGISVDSQSLH 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 DQQPHTQTASGQALKGDGGLYSSLP--PAKREEVEKLLNGSAGDTWRHLAGELGYQPEHI 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 LLLLLLGV-SLGGAKEA---CPTGLYTHSG-ECCKACNLGEGVAQPCGANQTVCEPCLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RSTPPEGSDSTAPSTOEPEAPPEODLIASTVAGVVITVMGSSOPVVTRGTIDN-LIPVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPC-----TEPCGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 PETQEAL--------CPQVTWSWDQLPSRALGPAAAPTLSPESPAGSPAMML-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: GDB:NGFR
A,Cross-references: GDB:120234; OMIM:162010
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 27, 2005, 13:37:13; Search time 176 Seconds (without alignments) 1213.279 Million cell updates/sec

US-10-081-280-6 2323 1 MEQRPRGCAAVAAALLLVLL......ERMGLDGCVEDLRSRLQRGP 417 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

	Description	Q93038 h tumor nec	Q99mm1 mus musculu	Q8vd70 mus musculu	P50555 sus scrofa	Q6qhf0 mus musculu	Q6qhf2 mus spretus	Q6qhfl mus musculu	-	P22934 rattus norv	019131 bos taurus		feli	077736 sus scrofa				Q9xs29 oryctolagus	Q76b99 xenopus lae	Q6glz4 xenopus lae	Q92956 homo sapien		O57408 meleagris g		Q9xsz8 cercopithec	Q9qzm4 mus musculu		-		Q9xs60 oryctolagus	Q71f55 mus musculu	Q9bdp2 macaca mula
SUMMARIES	ID	TR25 HUMAN	Q99MM1	Q8VD70	TRIA PIG	Q6QHF0	Q6QHF2	Q6QHF1	TRIA MOUSE	TR1A_RAT	TRIABOVIN	TRIA HUMAN	<u>095ND3</u>	TNR6_PIG	Q9TV <u>7</u> 9	Qenuue	Q861W6	Q9XS29	Q76B99	Q6GLZ4	TR14_HUMAN	Q9DFV0	057408	T10B_HUMAN	09XSZ8	T10B_MOUSE	TNR6 HUMAN	Q9IAR7	095185	09XX6O	Q71F55	TNR6_MACMU
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	Query Match Length	417	413	387	461	440	440	440	454	461	471	455	446	332	319	389	314	320	328	328	283	438	368	440	283	381	335	368	189	263	276	333
æ	Query	100.0	60.1	54.0	17.9	17.5	17.5	17.4	17.4	17.0	16.7	16.1	15.7	10.7	9.7	٠	9.5	9.4	9.5	9.1	٠	8.8	٠	8.8	٠	9.6	•	•	8.5	8.5	•	•
	Score	2323	1397	1255	415	406.5	405.5	404.5	404.5	394.5	387.5	374	365	247.5	226	223.5	221	217.5	214.5	211.5	206.5	205	203.5	203.5	200.5	200	199.5	199.5	198	198	197.5	197.5
	Result No.	-	~	m	4	ß	φ	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

097530 canis famil 097491 ovis aries 097491 ovis aries 097891 ovis aries 097846 mus musculu 0800000 muscaculu 066889 homo sapien 09940 macaca neme 099140 macaca neme 099141 xenopus tro 064181 xenopus tro 064181 xenopus tro 09bdn4 cercocebus 099079 gallus gall	
097530 097491 097584 TNR6 MOUSE 080WM 60SSE9 06SSE9 TNR6 MACNE 096140 06DJ81 06UXM 06DJ81 06UXM 06DJ81 06UXM 06ESTO	
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197 196.5 196.5 195.5 193.5 193.5 193.5 193.5 199.5 189.5	
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ALIGNMENTS

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TISSUE=Brain, and Fetal lung;
MEDLINE=97205313; PubMed=9052819;
Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
Browning J.L., Macdonald H.R., Tschopp J.;
"TRAMP, a novel apoptosis-mediating receptor with sequence homology to
tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARG-254.

Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,

Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,

Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;

"NIEMS-SNPS, envixonmental genome project, NIEMS ES15478, Department

of Genome Sciences, Seatle, WA (URL: http://egp.gs.washington.edu).";

submitted (MAR-2003) to the EMBL/GenBank/DbBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                              Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P. Baton D., Foster J., Grimaldi C., Guo C., Hass P.E., Heldens S., Lewis D., Kilm H.S., Kilmowski L., Jin Y., Johnson S., Lee J., Lee J., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M. H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A., improved the contraction of the contraction of the contraction of the contraction of the contractions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
Inliman R. T., Green R.E., Brenner S.E.;
"An unappreciated role for RNA surveillance.";
Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
-1-FUNCTION: Receptor for TNESF12/APO3L/TWEAK. Interacts directly with the adaptor TRADD. Mediates activation of NF-kappa-B and induces apoptosis. May play a role in regulating lymphocyte homeostasis.
                                                                                                                                                                                 "A new death receptor 3 isoform: expression in human lymphoid cell lines and non-Hodgkin's lymphomas."; Blochem. Biophys. Res. Commun. 242:376-379(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 11), AND VARIANTS GLN-23; GLY-159 AND
"LARD: a new lymphoid-specific death domain containing receptor
                                                                                         SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).
MEDLINE=98113360; PubMed=9446802; DOI=10.1006/bbrc.1997.7948;
Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
                                                                                                                                                                                                                                                                                              Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto
Hayashi S., Sato M., Shiozawa K., Tsukamoto Y.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chaudhary P.M., Hood L.E.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                       regulated by alternative pre-mRNA splicing.";
Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Senome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 7-417 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 4-417 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 283:543-546(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bioinformatics assessment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH BAG4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "ISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       death domains
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                                                                                                                                                                                                                                    -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=12;
Event=Alternative splicing; Named isoforms=12;
Name=1; Synonyms=wBL-1, LARD-1A;
Isold=Q93038-1; Sequence=Usp 006504;
Name=2; Synonyms=wBL-S1, LARD-3;
Isold=Q93038-2; Sequence=vSp 006504;
Name=3; Synonyms=wBL-S1, LARD-3;
Isold=Q93038-3; Sequence=vSp 006504;
Name=4; Synonyms=wBL-S2, LARD-2;
Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;
Name=4; Synonyms=LARD-4, LARD-1;
Isold=Q93038-4; Sequence=vSp 006502;
Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;
Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;
Isold=Q93038-5; Sequence=vSp 006495;
Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;
Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;
Name=7; Synonyms=LARD-5;
Isold=Q93038-7; Sequence=vSp 006491, vSp 006494;
Name=7; Synonyms=LARD-6;
Isold=Q93038-7; Sequence=vSp 006491, vSp 006494;
Name=7; Synonyms=LARD-6;
Isold=Q93038-7; Sequence=vSp 006491, vSp 006493;
Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;
Name=8; Synonyms=LARD-7;
Isold=Q93038-7; Sequence=vSp 006491, vSp 006493;
Name=8; Synonyms=LARD-7;
Isold=Q93038-8; Sequence=vSp 006491, vSp 006493;
Name=8; Synonyms=LARD-9;
Isold=Q93038-8; Sequence=vSp 006491, vSp 006493;
Name=8; Synonyms=LARD-9;
Isold=Q93038-8; Sequence=vSp 006491, vSp 006494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=9; Synonyms=LARD-8;
Name=10; Synonyms=LARD-8;
Name=10; Synonyms=LARD-9;
Name=110; Synonyms=Beta;
IsoId=093038-10; Sequence=VSP_006491;
Name=110; Synonyms=Beta;
IsoId=093038-110; Sequence=VSP_006496;
Name=11; Synonyms=Beta soluble;
IsoId=0931038-112; Sequence=VSP_006499; VSP_006500;
Note=May be produced at very low levels due to a premature stop note=May be produced at very low levels due to a premature stop—1: TISSUE SPECIFICITY: Abundantly expressed in thymocytes and lymphocytes. Detected in lymphocyte-rich tissues such as thymus, colon, intestine, and spleen. Also found in the prostate.
-!- SIMILARITY: Contains 1 death domain.
-!- SIMILARITY: Contains 4 TWFR-Cys repeats.
-!- CAUTION: Ref.5 reports for isoform 4 at position 208 a serine residue instead of arginine.
SUBUNIT: Homodimer. Interacts strongly via the death domains with TNFRSF1 and TRADD to activate at least two distinct signaling cascades, apoptosis and NF-Kappa-B signaling. Interacts with BAG4. SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9 and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)
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EMBL; Y09392; CAA70559.1; -.
EMBL: Y09392; CAA70560.1; -.
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U94502;
U94503;
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DEATH DOMAIN; 1.
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                    Query Match 60.1%
Best Local Similarity 62.9%
Matches 270; Conservative
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  PS50017;
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Name=Tnfrsf25;
                                                                                  SEQUENCE,
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                   PROSITE;
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PROSITE;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCB_TaxID=10090;
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homologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12)
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                                                              Length 417;
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Last annotation update)
                                                          100.0%; Score 2323; DB 1;
100.0%; Pred. No. 2.1e-153;
ive 0; Mismatches 0;
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GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
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InterPro; IPR011029; DEATH like.
InterPro; IPR001209; DEATH like.
InterPro; IPR006209; BGF like.
InterPro; IPR009130; Grow_fac_recept.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 1.
SWART; SW00005; DEATH; 1.
SWART; SW00208; TNFR; 2.
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EMBL; AF329969; AAK11256.1; -.
HSSP; P19438; 11CH.
EMBL; U94505; AAC51310.1; -. EMBL; U94506; AAC51311.1; -.
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                                                                             Best Local Similarity 100.
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KEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KETATALEFVB/N; TISSUE=Salivary gland;

KETATALEFVB/N; TISSUE=Salivary gland;

KETATALEFVB/N; TISSUE=Salivary gland;

KETATALEFVB/N; TISSUE=Salivary gland;

KALTATALEFVB/N; TISSUE=Salivary gland;

KALTATALEFVB/N; TISSUE=Salivary Glands G.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

Richards S., Worlley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
                                                                                                                                                                                                                                                                                          52
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                                                                                                                                                                                                                                                                                                                              53 AGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVAD
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                           28;
                                                                                                                                                               Length 413;
                                                                                                                                                            60.1%; Score 1397; DB 2; Length 4 62.9%; Pred. No. 4.6e-89; ive 28; Mismatches 103; Indels
PS01186; BGF_2; UNRNOWN 1.
PS00652; TNFR NGFR_1; UNRNOWN 1.
PS0050; TNFR NGFR_2; 1.
Y 413 AA; 44453 MW; 69F21B85D0DABABF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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Name=TNFRSF1A; Synonyms=TNFR1;
                                                                   SEQUENCE FROM N.A.
                                              NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                 67 RGCPKGHYMKAPCAEPCGNSTCLPCPSDTFLTRDNHFKTDCTRCQVCDEBALQVTLENCS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 FYEHGDGCVSCPISTLGSCPERCAAVCGWRQMFWVQVLLAGLVVVPLLLGATLTYTYRHCW 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 PCKAVVTADTAGTETLASPQTAHLSASDSAHTLLAPPSSTGKICTTVQLVGNNWTPGLSQ 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQEALCPQVTWSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRW 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCS 108
                                                                                                                                                                                                                                                                                                                                                                                                                              109 AVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------EAPT-----PLFWVQVLLG---VAFLFGAILICAYCRWQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHKPLVTADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKIC-TVQLVGNSWTPGYPE 287
                                                                                                                                                                                                                                                                                                                                           48
                                                                                                                                                                                                                                                                                                                                                               8 ERSPPGAATPGSTARVLQPLFLPLLLLLLLLLGGQGGGG-MSGRCDCASESQKRYGPFCC 66
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Genes S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                          EQRPRGCAAVAAA-------LLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCC
                                                                                                                                                                                                                                                                                                                      64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Tunor necrosis factor receptor superfamily member 1A precursor (p60)
                                                                                                                                                                                                                                                                                              54.0%; Score 1255; DB 2; Length 387; 57.7%; Pred. No. 3.2e-79; ive 26; Mismatches 92; Indels 64
                                                                                                        Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC017526; AAH17526.1; -.
R MGD; MGI:1934667; Tnfrsf25.
R GO; GO:0005615; C:extracellular space; TAS.
R GO; GO:0005615; C:extracellular space; TAS.
R GO; GO:0005615; C:integral to membrane; TAS.
R Pfam; PF00020; TNFR. C6; 1.
R SMART; SM00005; DaATH; 1.
R SMART; SM00005; DATH; 1.
R PROSITE; PS50017; DEATH DOMAIN; 1.
R PROSITE; PS50017; DEATH DOMAIN; 1.
R PROSITE; PS00165; EGF 2; UNKNOWN 1.
R PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1.
R PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1.
                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461 AA
                                                                                       SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE-Salivary gland;
                                                                                                                                                                                                                                                                                                         Best Local Similarity 57.7%
Matches 248; Conservative
                                                        and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TNF-R1) (TNF-RI) (p55).
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TD _TRIA_PIG

AC P5055;

DT 01-0CT-199

DT 01-0CT-199

DT 05-JUL-200

DE TUMOY TRIA_
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adjusting complex (DISC) performs caspase-8 protectly carrivation which initiates the subsequent cascade of caspases (asparente-specific cysteine proteases) mediating apoptosis (By similarity).

-!- SUBUNIT: Binding of TNF to the extracellular domain leads to homotrimerization. The aggregated death domains provide a novel molecular interface that interacts specifically with the death domain of TRADD. Various TRADD-interacting proteins such as TRAFS, RIP and possibly FADD, are recruited to the complex by their association with TRADD. This complex activates at least two distinct signaling cascades, apoptosis and NP-kappa-B signaling. Binds BAG4. Constitutively associated with TRPC4AP (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DOMAIN: Both the cytoplasmic membrane-proximal region and the C-terminal region containing the death domain are involved in the interaction with TRPC4AP (By similarity).
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               Gene 163:263-266(1995).
-!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
caspase-8 to the activated receptor. The resulting death-inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R EMBL; U19994; AAC48499.1; -.

R PIR; JC4302, JC4302.

R HSSP, P19438; 11CH.

R InterPro; IPR011029; DEATH like.

R InterPro; IPR011029; DEATH like.

R InterPro; IPR011029; DEATH like.

R Pfam; PF00020; TNFR C6; 3.

R MART; SM00005; DEATH; 1.

R SMART; SM00008; TNFR, 4.

R PROSITE; PS50017; DEATH DOMAIN; 1.

R PROSITE; PS50050; TNFR, 4.

R PROSITE; PS50050; TNFR NGFR 1; 3.

R APOPICOSIS; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                              MEDINE=9601645; PubMed=7590278; DOI=10.1016/0378-1119(95)00423-4; Suter B., Pauli U.H.; "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-SMase activation domain (NSD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor necrosis factor receptor
                                                                  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          superfamily member 1A.
Extracellular (Potential)
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Cytoplasmic (Potential).
TNFR-Cys 1.
TNFR-Cys 2.
TNFR-Cys 3.
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By similarity.
By similarity.
By similarity.
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65 DCPSPGRDTVCRECEKGTFTASQNYLR-QCLSCKTCRKEMSQVEISPCQADKDTVCGCK- 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 RHCWP-----HKPLVTADEAGMEALTPPPATHLSPLDSAHTLL-----APPDSSEK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----ENQFQRYLSETHFQCVDCSPC--FNGTVTIPCKETQNTVCNCHAGFFLRESECVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 TLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAHPQRPVNADLAI-----LYAVVDGVPPARWKEFMRFWGLSEHEIERLEMQNGRCLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 PCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 PISTLGSCP--ERCAAVC-----GWRQMFWVQVLLAGLVVPLLLGATLTYTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 ----SHCKKNEECMKLCLPPPLANVTNPQDSGTAVLLPLVILLGLCLLSFIFISLMCRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 PRWRPEVYSIICRDPVPVKEEKAGKPLTPAPSPAFSPTSGFNPTLGFSTPGFSSPVSSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 VAAALLLVLLGARAQGGT------RSPRCDCAGDFHKKIGLFCCRGCPAGHYLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
17.5%; Score 406.5; DB 2; Length 440; llarity 27.2%; Pred. No. 3.3e-20; Conservative 56; Mismatches 191; IndelB 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 QOYEMLKRWRQQQPA---GLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 AA; 48639 MW; D343ED449B260188 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                060HF2 PRELIMINARY; PRI; 440 cm. Q60HF2; 05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) TNF receptor superfamily, member 1A (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE, PSG0190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PSG0017; DEATH_DOMAIN; 1.
PROSITE; PSG1018; BGF 2; UNKNOWN_1.
PROSITE; PSG0052; TNFR_NGFR 1; 3.
PROSITE; PSG0050; TNFR_NGFR_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor.
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SEQUENCE
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Q6QHF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STLGSCPERCAAVCGWRQMP-----WVQVLLAGLVVPLLLGATLTYTYRHCWPH--- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 CKNADČKNLCPATSETRNDFQDTGTTVLLPLVIFFGLCLAFFLFVGLACRÝQRWKPKLYS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -------KPLVTADEAGMEALTPPPATHLSPLD--SAHTLLAPPDSSEKICTV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 QLVGNSWT----PGYPETQEALCPQVTWSWDQLPSRALGPAAAPTLSP-----ESPAG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 TFTPCDWSNIKVTSPPKEIAPPPQGAG-----PILPMPPASTPVPTPLPKWGGSAHSAHS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 VECQVSQCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPAMMLQPGP-QLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKR 381
                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 IICGKSTPVKEGEPEPLATAPSFG-----PITTFSPIPSFSPTTTFSPVPSFSPISSP
                                                                                                                                                                                                                                                                                                                                                                                                                                      VAPALLLIVILGARAQG-----GTRSPR---CDCAGDFHKKIGLFCCRGCPAGHYLKAPCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name-Tnfrøfla;
Nus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                       74;
                                                                                                                                                                                                                                              (GlcNAc. . .) (Potential) (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staelens J., Wielockx B., Puimege L., Vandenabeele A., Libert Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY541590; AA548429.1; -.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:005886; C:plasma membrane; TAS.
                                                                                                                                                                                                                                                                                                                                    17.9%; Score 415; DB 1; Length 461; 30.5%; Pred. No. 8.8e-21; tive 44; Mismatches 201; Indels
                                                                                                                                                                                                                                                                                          CD72361EC60C9D43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WRQ---QQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) TNF receptor superfamily, member 1A (Fragment)
    By similarity.
Nolinked (GlCNAC.)
N-linked (GlCNAC.)
N-linked (GlCNAC.)
N-linked (GlCNAC.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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STRAIN=C57BL/6JICO; TISSUE=Liver;
                                                                                               166 By 179 By 194 By 190 By 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                               Similarity 30.5
10; Conservative
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                                                                                                                                                                                                                                                                                               461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                       140;
                                                                            DISULFID
DISULFID
DISULFID
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                             ISULFID
ISULFID
ISULFID
                                                                                                                                                DISULPID
                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413
                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                   Local
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Matches
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119

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440
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SEQUENCE
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       셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 PCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 DCPSPGRDTVCRECEKGTFTASQNYLR-QCLSCKTCRKEMSQVBISPCQADKDTVCGCK- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 GWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : | : | | | : | | | | 177 ----SHCKKRQECMKLCLPPPLANVTNPQDSGTAVLLPLVILLGLCLLSFIFISLMCRY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 RH-----CWPHKPLVTADEAGMEALTPPPATHLSPLDSAHTLL-----APPDSS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 TPÍSPI-FGPSNWYFMPPVSEVVPTQGADPLLYESLCSVPAÞTFVQKWED-----PA- 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 ----ENÒFQRHLSETHFQCVDCSPC--FNGTVTIPCKETQNTVCTCHAGFFLRESECVPC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 PISTLGSCP--ERCAAVC-----GWRQMFWVQVLLAGLVVPLLLGATLTYTY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 EKICTVQLVGNSW------TPGY-PETQEALC----PQVTWSWDQLPSRALGPAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 APTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-F 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 VAAALLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCCRGCPAGHYLKA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 LSLVLLALLMGIHPSGVTGLVPSLGNŘEKRDSLČPQGKYVHSKNNSIČCTKČHKGTYLVS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97; Gaps
Name=Tnfrsfla;
Name=Tnfrsfla;
Bukaryota; (Western wild mouse).
Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=SPRET/Ei; TISSUE=Liver;
Staelens J., Wielockx B., Puimege L., Vandenabeele A., Libert
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 RDQQYEMLKRWRQQQPA---GLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.5%; Score 405.5; DB 2; Length 440; 28.1%; Pred. No. 3.8e-20; vative 56; Mismatches 184; Indels 97,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               440 AA; 48688 MW; 10E7ED7D289E0143 CRC64;
                                                                                                                                                                                                                                              EMBL; AYS41588; AAS48447.1; --
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0004015; F:receptor activity; IEA.
GO; GO:00040165; F:receptor activity; IEA.
GO; GO:0001165; F:receptor activity; IEA.
InterPro; IPR000345; CytC heme_BS.
InterPro; IPR000348; CytC heme_BS.
InterPro; IPR001349; Death.
InterPro; IPR00139; DEATH like.
InterPro; IPR00139; DEATH like.
Fam; PF00531; Death; I.
Ffam; PF00531; Death; I.
Ffam; PF00531; Death; I.
Ffam; PF00509; TNFR.c6; 3.
SMART; SM00005; DEATH; I.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN_I.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN_I.
PROSITE; PS00186; EGF Z; UNKNOWN_I.
PROSITE; PS001652; TNFR.NGFR.1; I.
PROSITE; PS00652; TNFR.NGFR.1; 3.
PROSITE; PS00652; TNFR.NGFR.2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440
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                                                                                                                                                         SEQUENCE FROM N.A.
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NON TER
NON TER
SEQUENCE
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  GG COCCOS AND THE TANK AND THE 
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440 AA

PRT;

PRELIMINARY;

Q6QHF1 JD Q6QHF1 RESULT 7

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60 PCTEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQASQVALENCSAVADTRCGCKP 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 ----ENÓFQRYLSETHFQCVDCSPC--FNGTVTIPCKETQNTVCNCHAGFFLRESECVPC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 PTSTLGSCP--ERCAAVC------GWRQMFWVQVLLAGLVVPLLLGATLTYTY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 RHCWP-----HKPLVTADEAGMEALTPPPATHLSPLDSAHTLL-----APPDSSEK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 PRWRPEVYSIICRDPVPVKEEKAGKPLTPAPSPAFSPTSGFNPTLGFSTPGFSSPVSSTP 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 ----SHCKKNEECMKLCLPPPLANVTNPQDSGTAVLLPLVILLGLCLLSFIFISLMCRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=DBA/2CrIBr; TISSUB=Liver;

STRAIN=DBA/2CrIBr; TISSUB=Liver;

SUBMITTED GRAD S. Pulmege L., Vandenabeele A., Libert C.;

SUBMITTED GRAD S. P. Pulmege L., Vandenabeele A., Libert C.;

BM 50, GO:005615; C:extracellular space; TAS.

GO; GO:005615; C:extracellular space; TAS.

GO; GO:005816; C:plasma membrane; TAS.

GO; GO:005816; C:plasma membrane; TAS.

GO; GO:005816; C:plasma membrane; TAS.

GO; GO:000516; P:tumor necrosis factor receptor binding; TAS.

RO; GO:000520; TNFR.GG; 3.

RO; GO:000516; P:tumor necrosis factor receptor binding; TAS.

RO; GO:000516; P:tumor necrosis factor receptor binding; P:tumor necrosis factor receptor binding; P:tumor necrosis factor receptor pinding; P:tumor necrosis factor receptor pinding; P:tumor necrosis factor necrosis factor necrosis factor necrosis factor necrosis factor necrosis factor necrosis fa
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440 AA; 48632 MW; 580A2D2E334612A3 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
1NF receptor superfamily, member 1A (Fragment).
Name-Tnfrsfla,
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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EMBL;
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  292 ISPI-FGPSNWHFMPPVSEVVPTQGADPLLYESLCSVPAPTSVQKWED------338
                                         315 TLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIBAVEVEIGR-FRD 373
                                                                   339 SAHPQRPDNADLAI-----LYAVVDGVPPARWKEFMRFWGLSEHEIERLEMQNGRCLRE 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91187885; PubMed-1849278; Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chem E.Y., Goeddel D.V.; Pub. 1. "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92039815; PubMed=1657766;
Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
"Molecular cloning and expression of the mouse Tnf receptor type b.";
"Immunogenetics 34:338-34(1991).
                                                                                                                                                                                                                                                                                                                                      ol-May-1992 (Rel. 22, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 1A precursor (p60)
(TWF-RL) (TWF-RL) (P55).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-93156721; Pubmed-8381516; DOI=10.1016/0161-5890(93)90088-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

BEDLINES-1246168; PubMed=1645445;
GOGGWin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
Copeland N.G., Jenkins N.A., Smith C.A.;
Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.";
Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-91285014; PubMed=1647956; MEDLINE-91285014; PubMed=1647956; MEDLINE-91285014; L.Y. Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M., Gray P.W., Feldmann M., Foxwell B.M.J.; Gray P.W., Feldmann M. Foxwell B.M.J.; "Cloning, expression and cross-linking analysis of the murine p55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.; "Genomic organization and promoter function of the murine tumor necrosis factor receptor beta gene."; Mol. Immunol. 30:165-175(1993).
                                                                                                                                    417
                                                                                                                                                            Bebo B.F., Linthicum D.S.; "Nucleotide sequence of the TNF type I receptor from a mouse
                                                                                                                                374 QQYEMLKRWRQQQPA---GLGAVYAALERMGLDGCVEDLRSRLQRGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
                                                                                                                                                                                                                                                                                            454 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Tnfrsfla; Synonyms=Tnfr-1, Tnfr1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumor necrosis factor receptor.";
Eur. J. Immunol. 21:1649-1656(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94245292; PubMed=8188324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endothelioma cell line.";
Immunogenetics 39:450-451(1994).
                                                                                                                                                                                                                                                                                                                                   (Rel. 22, Created)
                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                   01-MAY-1992
                                                                                                                                                                                                                                                                                         TRIA MOUSE
P25118;
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STRAIN=C3H/He; TISSUE=Mesenchyme;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Astaubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Astaplecton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Pecers G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEvan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raha S.S., Letteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 In mouse Comparison of the Action of Transport of the Action of Transport of Transp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1314884; Tnfrsfla.
MGD; MGI:1314884; Tnfrsfla.
MGO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.
GO; GO:0006952; P:defenser response; IMP.
GO; GO:0006954; P:inflammatory response; IMP.
GO; GO:0007515; P:lymph gland development; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein.

DOWAIN: Both the cytoplasmic membrane-proximal region and the C-terminal region containing the death domain are involved in the interaction with TRECARP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1'death domain.
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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EMBL, M76656; AAA40465.1; --
EMBL, M88067; AAA40465.1; JOINED.
EMBL, M76655; AAA40465.1; JOINED.
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InterPro; IPR011029; DEATH like.
InterPro; IPR001368; TNFR_G6.
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X59238;
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LEW/NHsd;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345 SAHPQRPDNADLAI-----LYAVVDGVPPARWKEFNRFMGLSEHEIERLEMQNGRCLRE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 VAAALLLVLLGARAQGGT-----RSPRCDCAGDFHKKIGLFCCRGCPAGHYLKA 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity.
By sim
PFONOID: TNFR C6; 4.

PROSITE; PSS0017; DEATH DOMAIN; 1.

PROSITE; PSS0052; TNFR WGFR 1; 3.

PROSITE; PSS0050; TNFR WGFR 2; 3.

Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane. SIGNAL 1

21 Potential.

CHAIN 22 454 Tumor necrosis factor recent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-SMase activation domain (NSD).
Death.
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                                                                                                                                                                                                                                                                                                                                 Extracellular (Potential)
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0710C2E8C3C2B6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential).
TNFR-Cys 1.
                                                                                                                                                                                                                                                                                       superfamily member 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNFR-Cys 2.
TNFR-Cys 3.
TNFR-Cys 4.
                                                                                                                                                                                                                                                                                                                                                                    Potential.
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50129 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 127; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             399
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DISULFID
DISULFID
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 PTSTLGSCP--ERCAAVC-----GWRQMFWVQVLLAGLVVPLLLGATLTYTYR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFLGLCLLFFICISLLCRYP 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.0%; Score 394.5; DB 1; Length 461; 27.9%; Pred. No. 2.3e-19; ive 55; Mismatches 202; Indels 73; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NHSd).

H -> P (in strain LEW/NHSd, strain ACI/SegHed, strain DA/Bkl, strain F344/NHSd and strain BN/SSNHSd).

EB23C05450FBD202 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (in strain LEW/NHsd, strain ACI/
                                                                                                                                                                                                                                                                                                                                     TWRR-Cys 3.

TWRR-Cys 4.

N-SMase activation domain (NSD).
Death.
By similarity.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SegHsd, strain DA/Bkl and strain F344/
NHsd).
                                                                                                          Repeat; Signal; Transmembrane.
                                                                                                                                                         Tumor necrosis factor receptor
                                                                                                                                                                                    superfamily member 1A.
Extracellular (Potential).
                                                                                                                                                                                                                                                                 Cytoplasmic (Potential).
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                                                                                                                                                                                                                                                                                         TNFR-Cys 1.
TNFR-Cys 2.
                                                                                                                                                                                                                                        Potential
                                                                                                  Apoptosis; Glycoprotein; Receptor; Rep
SIGNAL 1 21 Potential
CHAIN 22 461 Tumor nec
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SMART; SM00208; INFR; 4.
PROSITE; PSS0017; DEATH DOMAIN; 1.
PROSITE; PS00052; INFR_NGFR_1; 3.
PROSITE; PS50050; INFR_NGFR_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 AA; 50969 MW;
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Matches 128; Conservative
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**MEDLINE=98273505; PubMed=9613449; DOI=10.1016/S0165-2427(97)00136-0; Lee E.-K., Kehrli M.E. Jr., Taylor M.J.; Lee E.-K., Kehrli M.J.; Lee E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DR InterPro; IRR001450; Death.

DR InterPro; IRR001029; Death.

IR InterPro; IRR01029; DEATH.

DR InterPro; IRR01039; DEATH.

IR Ffam; PF00031; Death, 1.

DR Ffam; PF00030; TWRR C6; 3.

R FRINTS; PR00035; 4FE4SFRDOXIN.

R SMART; SM00006; DEATH; 1.

R SMART; SM00206; DEATH; 1.

R RR0SITE; PS00017; DEATH DOMAIN; 1.

R PROSITE; PS00052; TWRR NGFR 1; 3.

R PROSITE; PS00050; TWRR NGFR 2; 3.

R PROSITE; PS0050; TWRR NGFR 2; 3.

R PROSITE; PS0050; TWR NGFR 2; 3.
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SIMILARITY: Contains 1 death domain.
SIMILARITY: Contains 4 TNFR-Cyg repeats.
                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
17-Wmor necrosis factor receptor superfamily member 1A precursor (p60)
(TNF-R1) (TNF-R1) (p55).
Name=TNFRSF1A, Synonyms=TNFR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                       471
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                                                                                                                                                                                                                                                                       STANDARD;
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factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.";
DNA Cell Biol. 9:705-715(1990).
                                                                                                                                                                                                                                                                                Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W., Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.; "Molecular cloning and expression of a receptor for human tumor necrosis factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201. MEDLINE=91006021; PubMed=1698610; Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R., Aderka D., Holtmann H., Wallach D.; Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor receptor superfamily member 1A precursor (p60)
Tumor necrosis factor (D50) (CD120a) (COntains: Tumor necrosis factor binding protein 1 (TBP1)).
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90235284; PubMed=2158862; Lothar R., Gentz R., Brockhaus M., Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M., Tabuchi H., Lesslauer W., "Molecular cloning and expression of the human 55 kd tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91090841; PubMed=1702293; Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier Lante M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.; Molecular cloning and expression of human and rat tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANTS LEU-75 AND GLN-121.
Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A., Rajkumar N.R., Toth B.J., Yi Q., Nickerson D.A.,
"SeattleSNPs. NHLBI HL6622 program for genomic applications, UW-FHCRC, Seattle, WA (URL. http://pga.gs.washington.edul.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.; "Cloning of human tumor necrosis factor (TNR) receptor cDNA and expression of recombinant soluble TNR-binding protein."; proc. Natl. Acad. Sci. U.S.A. 87:7380-7384
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92250049; PubMed=1315717;

Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;

"Structure of the human TNF receptor 1 (p60) gene (TNFR1)

localization to chromosome 12p13.";
                                                                                             binding protein 1 (TBPI)].
Name=TNFRSF1A; Synonyms=TNFAR, TNFR1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placenta;
MEDLINE=91017509; PubMed=2170974;
                                                                                                                                                                                                                                               TISSUE=Placenta;
MEDLINE=90235285; PubMed=2158863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics 13:219-224(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 9:3269-3278(1990).
                                                                                                                                                                                                                                                                                                                                                          Jell 61:361-370(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell 61:351-359(1990)
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                         WCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             actor receptor.
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   18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 KPGWFVECQVSQCVSSSPFYCQPCLDC--GALHRHTRLLC-SRRDTDCGTCLPGFYEHGD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 RKN----QYREYWGETGFRCLNCSLCPNGTVN----IPCQERQDTIC-HCHMGFFLKGA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 KCISC----HDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 PQVTWSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354 LGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVEDL 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 VLPALLADVYPAGVÓGLVPHP----GDLEKRESPCPQGKYNHPQNSTICCTKCHKGTÝL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 KAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 YNDCPGPGRDTDCRVCAPGTYTALENHIR-RCLSCSRCRDEMFQVBISPCVVDRDTVCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 GCVSCPTSTLGSCPER-CAAVCGWR------QMFWVQVLLAGLVVPLLLGATLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 ADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNS--WTPGYPETQEALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 VAAALLLVLLGARAQGGTRSPRCDCAGDF------HKKIGLFCCRGCPAGHYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 121; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 GlcNAc. . .) (Potential) (GlcNAc. . .) (Potential) (GlcNAc. . .) (Potential)
                                                                      Cytoplasmic (Potential).
TWFR-Cys 1.
TWFR-Cys 2.
TWFR-Cys 3.
TWFR-Cys 4.
N-SMase activation domain (NSD).
Death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.7%; Score 387.5; DB 1; Length 471; 26.9%; Pred. No. 7.3e-19; ive 47; Mismatches 186; Indels 121.
necrosis factor receptor
                                     Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5243EF514DFE81C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 YTYRHCWPHK-------
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similarity.
similarity.
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                                                                                         Best Local Sim.
Matches 130;
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TRIA HUMAN ID TRIA HI AC P19438

RESULT 11

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X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB. MEDLINE=93258809; PubMed=8387891; DOI=10.1016/0092-8674(93)90132-A; Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J., Broger. C., Loestscher H., Lesslauer W.; Crystal structure of the soluble human 55 kd TNF receptor-human TNF beta complex: implications for TNF receptor activation."; Cell 73:431-445(1993).
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Evidence for immunological cross-reactivity with cell surface tumor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Naismith J.H., Devine T.Q., Khono H., Sprang S.R.; Hanor necrosis "Structures of the extracellular domain of the type I tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=99115917; PubMed=9915703; DOI=10.1126/science.283.5401.543; Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.; Woronicz J.D., Liu W., Goeddel D.V.; "Prevention of constitutive TNF receptor 1 signaling by silencer of
Feingold E.A., Grouse L.H., Derge J.G.
                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        necrosis factor receptors.";
J. Biol. Chem. 265:1531-1536(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97094982; PubMed=8939750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory syndromes.";
97:133-144(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structure 4:1251-1262(1996)
                                                                                                                                                                                                                                                                                                                 mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 283:543-546(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERACTION WITH BAG4.
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 41-45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  death domains
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**New Natural Fire Ser. 39.

**New Natural Fire Ser. 39.

**Augulara K.*, Nomura A., Nakao F., Hara T.;

**Rusuhara K.*, Nomura A., Nakao F., Hara T.;

**Rusuhara K.*, Nomura A., Nakao F., Hara T.;

**Tumour necrosis factor receptor-associated periodic syndrome with a novel mutation in the TNFRFIA gene in a Japanese family.";

**Lur. J. Pediatr. 163:30-32(2004).

**Lur. J. Pediatr. 104 Tumbor. The and one cremitic acceptor for the activation of TRADD. Interacts specifically with the death domain of TRADD. Various TRADD-interacting proteins such as TRAFS, the procession of The complex by their association with TRADD. This complex activates at least two distinct signaling cascades, apoptosis and NP-kappa-B signaling. Similar Larious. The suppression of the complex by their signaling cascades, apoptosis and NP-kappa-B signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 EC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSTLGSCPE--RCAAVC-----GWRQMFWVQVLLAGLVVPLLLGATLTYTYRH 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 ----SNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 HYWSENLFOC----FNCSLCLN-GTVH----LSCOEKONTVCTCHAGFFLRENECVSC- 182
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                                                                                                                                                                                                                                                               VARIANTS FHF SER-99 AND PRO-121.

PubMed=13130484; DOI=10.1002/art.11215;

PubMed=13130484; DOI=10.1002/art.11215;

PubMed=13130484; DOI=10.1002/art.11215;

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Manna R., Powell R.J., Woo P., Solis P., Minden K., Frenkel J.,

Yague J., Mirakian R.M., Hitman G.A., McDermott M.F.;

"Heterogeneity among patients with tumor necrosis factor receptor-
associated periodic syndrome phenotypes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 LLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPONNSICCTKCHKGTYLYNDCPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 PCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQASQVALENCSAVADTRCGCKPGWFV
                                                       Aksentijevich I., Galon J., Soares M., Mansfield E., Hull K., Oh H.-H., Goldbach-Mansky R., Dean J., Athreya B., Reginato A.J., Henrickson M., Pons-Estel B., O'Shea J.J., Kastner D.L.; "The tumor-necrosis-factor receptor-associated periodic syndrome: new mutations in TNFRSF1A, ancestral origins, genotype-phenotype studies, and evidence for further genetic heterogeneity of periodic fevers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 LILLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.1%; Score 374; DB 1; Length 455;
28.3%; Pred. No. 6.1e-18;
tive 49; Mismatches 183; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SUBCELLULAR LOCATION: Type I membrane protein and secreted.
DOMAIN: The domain that induces A-SMASE is probably identical to
the death domain. The N-SMASE activation domain (NSD) is both
necessary and sufficient for activation of N-SMASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ပ်
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                     VARIANTS FHF GLN-51; SER-59; GLY-62; LEU-75; GLY-115 AND GLN-121
                                            PubMed=11443543;
Aksentijevich I., Galon J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

L. FUNCTION: Receptor for INFSE6/FASL. The adaptor molecule FADD

recruits caspase-8 to the activated receptor. The resulting death-
inducing signaling complex (DISC) performs caspase-8 proteolytic

activation Which initiates the subsequent cascade of caspases

(aspartate-specific cysteine proteases) mediating apoptosis. FAS-
mediated apoptosis may have a role in the induction of peripheral

colerance, in the antigen-stimulated suicide of mature T-cells, or
both (By similarity).

colerance, in the antigen-stimulated suicide of mature T-cells, or
both (By similarity).

colerance and maybe to other cytosolic adaptor proteins.

colerance and maybe to other cytosolic adaptor proteins.

colerance and maybe to other cytosolic adaptor proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                             183 TLGS-CPERCAAVC-----GWRQMFWVQVLLAGLVVPLLLGATLTYTYR----- 225
                                                                                                                                                                                                                                    278 GNSWIPGYPETQEALCPQVTWSWDQL------PSRALGP--AAAPTLSP----- 318
                                                                                                                                                                                                                                                                 ::||
--TFTPS------DWANLRAASVSREMAPPYQGAGPILSAAPASSPISTPVQ 329
                                                                                                                                                                                                                                                                                                                                      -----ESPAGSPAMMLOPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR 370
                                                                                                                                                                                                                                                                                                                                                                      330 KWEDSTHIQRPEADPA---DPA-TLYAVVDGVPPSRWKEFVRRLGLSEHEIERLELQNGR 385
                                                                             186 KKNTECTKLCVPIVETVKDPQDPGTTVLLPLVIFFGICVLSFSIGLMCRYQRRKSKLFSI
                                                                                                                                  ---HCWPHK-----PLVTADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D., "Expression of apoptosis-associated genes in hibernating and stunned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  precursor (FASL (Apo-1 antigen)
                                                                                                                                                                                 246 VCGKSTPTKEGEPQPLATG----PGFSPIPSP---SPTFTPSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         371 -FRDQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVEDLRSRL 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 CLKEAHYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEAL 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.UUL-1999 (Rel. 38, Last sequence update)
2.cor-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 preceptor) (Apoptosis-mediating surface antigen FAS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000488; Death.
InterPro; IPR011029; DEATH like.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00531; Death; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=TNFRSF6; Synonyms=APT1, FAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ001202; CAA04596.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P25445; 1DDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CD95 antigen)
                                                                                                                                                                                                                                                                                      286
                                                                                                                                                                                                                                                                                                                                         319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNR6_PIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 QKWEDSAHKPQSLDIDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGRCLRE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---AHTLLAPPDSSEKIC 272
                               239 -WKSKLYSIVCGKSTPEKEGELEGTTTKP---LAPNPSFSPTPGFTPTLGFSPVPSSTFT 294
                                                                                                    273 TVQLVGNSWTPGYPETQEALCPQVTWSWDQLPSRALGP------AAAPTLSP- 318
                                                                                                                                                    S----SSTYTPGD-----CPNFA----APRREVAPPYQGADPILATALASDPIPNPL 338
                                                                                                                                                                                                       319 ---ESPAGSPAMMLOPGP-QLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRD 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 EPCGNSTCLVCPQDTFLAWENHINSECARCQACDEQASQVALENCSAVADTRCGCKPGWF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---OYRYYWSETHFOCLNCSLC--INGTVOISCKETONTVCTCHAGFFLRGNECVSCVNC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 VAAALLLVLLGARAQG-----GTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 VLLALLVEIYPLRVTGLVPHLRDREKRAIPCPQGKYIHPQDNSICCTKCHKGTYLYNDCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=2145403; PubMed=11531421; DOI=10.1006/viro.2001.1042; Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.; Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.; InTNF-alpha-induced cell death in feline immunodeficiency virus-infected cells is mediated by the caspase cascade."; Virology 287:446-455(2001).

EMBL; AB051103; BAB55455.1; --
HSEP; P19438; 11CH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.7%; Score 365; DB 2; Length 446; 27.0%; Pred. No. 2.5e-17; Live 45; Mismatches 184; Indels 1:
                                                                                                                                                                                                                                                                                                         374 QOYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVEDLRSRL 413
                                                                                                                                                                                                                                                                                                                                         399 AQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEAL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217BD331DD8A74AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
227 CWPHK-----PLVTADEAGMEALTPPPATHLSPLDS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005515; F:protein binding; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007165; F:receptor activity; IEA.
GO:0007165; F:receptor activity; IEA.
INCEPPO: IPRO00345; CytC heme_BS.
INCEPPO: IPRO1029; Death.
INCEPPO: IPRO06209; EGF like.
INCEPPO: IPRO06209; EGF like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS00186; DEGF 2; UNKNOWN 1.
PROSITE; PS00652; TNFR NGFR 1; 3.
PROSITE; PS50050; TNFR NGFR 2; 3.
SEQUENCE 446 AA; 49563 MW; 217BD331DD8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor necrosis factor type I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00531; Death; 1.
Pfam; PF00020; TNFR C6; 3.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=TNFR I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126;
                                                                                                                                                    295
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Matches
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Q95ND3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 ECPEGOHRE-GOPCCOPCPPGKRKHADCTSPGGAPQCVPCSEGEDYTDKNHHSSKCRRCR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 ACDEQASQVALENCSAVADIRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 LCSRRDTDCGTCLPGFYEHG--DGCVSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLV 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------EHGVIENCT--PTSNT-KCREVFQSAGSRSNLHWLWALLILIP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 DCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQ 93
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
10.7%; Score 247.5; DB 1; Length 332;
Best Local Similarity 30.3%; Pred. No. 2.7e-09;
Matches 56; Conservative 23; Mismatches 67; Indels 39; Gaps
                                                                                                                                                             Cytoplasmic (Potential).

TNFR-Cys 1.

TNFR-Cys 2.

TNFR-Cys 3.

Death.

By similarity.

N-linked (GlCNAC. . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B-type Fas antigen.
Oytotolagus cuniculus (Rabbit).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
Pfam; PF00020; TNFR_C6; 3.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00005; DEATH; 1.
SMART; SM01005; TNFR; 3.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS50052; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
SIGNAL
                                                                                                                  Tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Isono T., Tanbe Y., Nagano Y., Seto A.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AB021299; BAA78430.1; -.
HSSP; P25445; IDDF.
                                                                                                                                                                                                                                                                                                                                                                   linked (GlcNAc. . .) (Pc
5B8B03682756BF1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0016620; C:membrane; IEA.
GO:0005515; F:protein binding; IEA.
GO:0004888; F:transmembrane receptor activity; IEA.
                                                                                                                              superfamily member 6.
Extracellular (Potential)
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                            37592 MW;
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                                                                                                                                                                                                                                                                                                                                                                            332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 VPLLL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 VPALV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9986;
                                                                                                                                          DOMAIN
TRANSMEM
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DISULFID
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DISULFID
DISULFID
                                                                                                                                                                               REPEAT
REPEAT
REPEAT
DOMAIN
DISULFID
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                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                             DISULFID
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                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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GNFCCQLCPPGTKKKADCTSNEGKPDCEPCQEGEEYTDKSHFSSKCRRCSLCDGEHGLEV 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 YRHCWPHKPLVTADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 GYPETQEALCPQVTWSWDQLPSRALGPAAAP----TLSPESPAGSPAMMLQPGPQLYD 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 GYDK-----STALIPEGVPMNFSDVDISKYIPT------ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 LENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 TCLPGFYEHGDGCVSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshlyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Millahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.7%; Score 226; DB 2; Length 319;
Best Local Similarity 21.0%; Pred. No. 8.2e-08;
Matches 73; Conservative 42; Mismatches 103; Indels 130; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; (wanio rerio).
Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 VMDAVPARRWKEFVRTLGLREAEIEAVEVE-IGRFRDQQYEMLKRWRQ 384
GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0006955; P:immune response; IEA.

GO; GO:0007165; P:aignal transduction; IEA.

InterPro; IPR001029; DEATH—like.

InterPro; IPR001029; DEATH—like.

InterPro; IPR0010369; TNFR_C6.

Pfam; PF00520; TNRR_C6; 2.

Pfam; PF00500; TNRR_C6; 2.

RPMINTS; PR01060; PAŠRECBFTOR.

SWART; SW000009; TNFR; 3.

RPROSITE; PS50017; DEATH DOMAIN; 1.

RPOSITE; PS50017; DEATH DOMAIN; 1.

RPOSITE; PS50017; DEATH MGFR_1; UNKNOWN—1.

RPOSITE; PS50017; DAATH MGFR_1; UNKNOWN—1.

RPOSITE; PS50017; DAATH MGFR_1; 0.05FA0033B1846591 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 LRRYKKHR-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OřFNames=zgc:85914;
Brachydanio rerio (Zebrafish) (Danio rerio)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --QVSQCVSSSPFYCQPCLDCGALH----RHTRLLCSRRDTDCGTCLPGFYEHGDGC--- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --VSCP----TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPH 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 KPLVTADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 ALCPQVTWSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEF 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRTLGLREAEIEAVEVEIGRFRDOQYEMLKRWRQQQPAG-----LGAVYAALERMG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 CKTSIPPVFFTSTKSNSPEDTVPK-----IVVPVCASIMVLSLAIFMAYEGIRHWRK 233
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; Green E.D., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; Green E.D., Grimwood J., Schnerch S.J., Marra M.A.; Green E.D., Schnerch A., Schein J.E., Jones C.DNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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larity 21.8%; Pred. No. 1.5e-07;
Conservative 60; Mismatches 158; Indels 119.
                                                                                                                                                                                                                                              Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC068424; AAH68424.1;
ZFIN; ZDB-GENE-040426-2252; zgc:85914.
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0004872; F:receptor activity; IEA.
R InterPro; IPR00145; P:signal transduction; IEA.
R InterPro; IPR00145; AF645 ferredoxin.
R InterPro; IPR00148; Death.
R InterPro; IPR01029; DEATH like.
R InterPro; IPR01288; TNFR_G6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00531; Death; 1.
Pfam; PF00031; Fer4; 1.
Pfam; PF00020; TNFR_c6; 3.
SMART; SM00208; DTATH; 1.
SMART; SM00208; TNRR; 3.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
PROSITE; PS00052; TNRR NGFR_1; UNKNOWN_2.
PROSITE; PS00652; TNRR NGFR_1; UNKNOWN_2.
SROUENCE 389 AA; 44099 MW; 9EB46F454519FB3C CRC64;
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Search completed: June 27, 2005, 13:40:20 Job time : 179 secs

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Death domain containing receptor polypeptide(s) DR3 and DR3-V2 - for activation of apoptosis and NF-kappaB, antagonists can be used to treat inflammatory diseases.
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Aaw55709 Human apo
Aaw55704 Human apo
Aaw55245 Human dea
Aab58265 Human rhe
Aab58265 Human rhe
Aab7370 Human rhe
Aau61399 Human RRO
Abu08252 Human Apo
Abu08252 Human Apo
Aby73893 Human Apo
Aby73893 Human Apo
Aby73893 Human Apo
Aby73894 Human Apo
Ada465969 Human apo
Ada465969 Human BEC
Adh36829 Human Gaa
Adh36829 Human BEC
Adh36829 Human Gea
                                                            June 27, 2005, 13:37:14 ; Search time 164 Seconds (without alignments) 983.409 Million cell updates/sec
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                                                                                                                  2323
1 MEQRPRGCAAVAAALLLVLL......ERMGLDGCVEDLRSRLQRGP
5.1.6
Compugen Ltd.
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GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2002s:*
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geneseqp2003bs:*
geneseqp2004s:*
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Perfect score:
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Maximum DB 6
                                        OM protein
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Aab64941 Amino aci Adh50948 Human dea Aab64486 Human DR3 Abg7395 Human DR3 Ad15011 Human W5L Abm84914 Human dia Abm84915 Human dia Aaw31516 Death dom Aaw35537 Death dom Aab56264 Human DB3 Ad127891 Human DB3 Ad127891 Human DBA Aab50918 Human PRO Aab510009 Human PRO Ad115009 Human W5L Ad115010 Human W5L Ad115010 Human W5L Ad115010 Human W5L Ad115010 Human M5L Ad15010 Human APO	m	V1; human; apoptosis; inflammation; domain" domain" lon PJ;
4 AAB84941 8 ADH50948 2 AAW64486 6 ABG73995 6 ABG73995 7 ADL15011 8 ABM84914 8 AAM95537 2 AAW31516 2 AAW31516 2 AAW31516 3 AAB01337 4 AAB50918 2 AAW57046 7 ADL15009 7 ADL15009 6 ABG73992	ALIGNMENTS in; 417 AA. y) receptor DR3.	lifiers lifiers peptide acellular smembrane acellular h domain"
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199. .224
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/label= Sig_peptide
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Matches 417; Conservative
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indices apoptotic activity in mammalian cells purposes. Its amino acid sequence was deduced from a human foetal heart cDNA clone (see AAF91180).

Crancher novel apoptosis polypeptide, Apo-211 (see AAFA5709). Also claimed another novel apoptosis polypeptide, Apo-211 (see AAFA5709). Also claimed are: polypeptides comprising the extracellular or death domain of Apo-3; chimeric molecules comprising Apo-3 fused to a heterologous amino acid sequence; antibodies that bind to Apo-3 or its extracellular domain; cells; a non-human transgenic animal containing cells that express culls; a non-human transgenic animal containing cells having an altered Apo-3 gene. Apo-3 can be used to induce apoptosis or NF-kB induction or JNK mediated gene expression for therapeutic purposes. Apo-3-1gG fusion proteins can be used to inhibit apoptosis or NF-kB induction or JNK activation for therapeutic purposes, and can be used as immunogens for anti-Apo-3- antibody production. Apo-3 or Apo-2011 can also be used as assay standards. The animals can be used in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This novel polypeptide, designated Apo-3, is a protein that stimulates or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WFVECOVSOCVSSSPFYCOPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP
                                                                                                                                                                                                                                                                                                                                                                                        Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis in mammalian cells.
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 /note= "transmembrane domain"
                  225. .417
/note= "intracellular domain"
                                                 338. .417
/note= "death domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 19; Page 46-48; 70pp; English.
                                                                                                                                                                             97WO-US005230.
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96US-00710802.
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Matches 417; Conservative
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The invention provides nucleotide sequences encoding death domain containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is contained in ATCC deposition No. 97757. Recombinant vectors comprising the nucleic acid sequences and optionally the leader sequences are used for the recombinant production of the proteins. The present sequence represents the amino acid sequence of a death domain containing receptor
241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
                                                                                                                                                     MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
                                                                                                                                  DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New death domain containing receptor and recombinant vector - optionally
                                                                                                                                                                                                                             361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Death domain containing receptor polypeptide (DR3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Death domain; receptor; DR3-V1; DR3; recombinant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25. .417
/note= "mature protein"

    .24
    note= "signal peptide"

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96US-0028711P.
97US-0037341P.
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Best Local Similarity 100.
Matches 417; Conservative
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06-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is the human apoptosis inducing receptor (AIR) of the invention. AIR is a Type I transmembrane protein, soluble forms of which can be used to regulate cell death in a therapeutic setting. Soluble AIR can be used to ritro to block apoptosis or AIR-expressing cells, or to screen agonists or antagonists of AIR activity. The cytoplasmic domain of AIR can be used to develop assays for inhibitors of AIR-induced cell death, which is useful to regulate cell death in a therapeutic setting as well as in vitro. Agonists of AIR activity can be used to kill tumour cells that express AIR, or I cells expressing AIR in autoimmune diseases
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121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
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                                                                             417
                                                                                                                                                                                                                                                                                                                                    Apoptosis inducing receptor; AIR protein; human; cell death regulator; Type I transmembrane protein; tumour cell death; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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                                                          IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding apoptosis inducing receptor - protein, useful for regulating cell death.
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                                                                                                                                                                                                                                                                                                   Human apoptosis inducing receptor.
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Matches 417; Conservative
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N-PSDB; AAV28700.
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                                                                                                                                                                                241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
                                              CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                                                       TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
                                                                                                                                     DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                                                                                                                                                                                                           DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                  CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                             WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                 121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                   MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
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                                                                                                                                                                                                                                                         361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                                                                                                                                                                      Identifying agonists and antagonists of tumor necrosis factor related receptors TR1, TR3 and TR5, and of ligand TL3, useful for treatment of cancer, AIDS, Alzheimer's disease, bone disease etc.
                                                                                                                                                                                                                                                                                                                                                                                                                           agonist;
Tumour necrosis factor receptor; TR3; DR3; Apo3; WSL-1; LARD; agonist antagonist, screening; human, Alzheimer's disease; ALDS; cancer; inflammation; arthritis; septicaemia; autoimmune disease; psoriasis; inflammatory bowel disease; transplant rejection; graft versus host disease; inflection; stroke; ischaemia; acute respiratory disease syndrome; restenosis; brain injury; bone disease; atherosclerosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 12-13; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Tumour necrosis factor receptor TR3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-246560/21.
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to the receptors or ligand, and which activate (agonist) or inhibit activation of (antagonists) TR1, TR3, TR5 or TL3. A screening kit for identifying agonists, antagonists, ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or TL3 polypeptides is provided. The agonists and antagonists are useful for treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune disease e.g. inflammatory bowel disease, psociaais, transplant rejection, graft versus host disease, infection, stroke, ischaemia, acute respiratory disease hymphoproliferative disorders), atherosclerosis, brain injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders), atherosclerosis, Alzheimer's disease, etc., caused by imbalance of TR1, TR3, TR5 or TL3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTEPCGNSTCLVCPQDTFLAWENHINSECARCQACDEQASQVALENCSAVADTRCGCKPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEORPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCCRGCPAGHYLKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 2323; DB 2;
100.0%; Pred. No. 1.3e-161;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; death domain containing receptor; DR3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human death domain containing receptor DR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurodegenerative disease; angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0136741P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 417; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 417 AA;
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This invention relates to a method of diagnosing chronic rheumatoid arthritis by digesting human genomic DNA with ECORI and hybridising it with a probe for the DNA encoding the present protein which is a rheumatoid arthritis associated transmembrane protein. The method is used for the diagnosis of chronic rheumatoid arthritis, and for developing new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
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                                                                                                                                                                                                                                                                                                         Diagnosing rheumatoid arthritis by probing digested human genomic DNA or comparing expression of mRNA or polypeptide of a region of transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 2323; DB 4; Length 417; 100.0%; Pred. No. 1.3e-161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
 Rheumatoid arthritis; transmembrane protein; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 15-17; 21pp; Japanese.
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                                                                                                                              01-NOV-2000; 2000WO-JP007690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 417; Conservative
                                                                                                                                                                                                                            Konishi
                                                                                                                                                                                                                                                         WPI; 2001-308750/32
N-PSDB; AAH27782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                              SHIO/) SHIOZAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 417 AA;
                                                               WO200132921-A2
                                   Homo sapiens
                                                                                                                                                              01-NOV-1999;
                                                                                                                                                                                                                            Shiozawa S,
                                                                                               10-MAY-2001
                                                                                                                                                                                                                                                                                                                          comparing
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                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences for two death domain containing receptors, designated DR3 and DR3-V1. These receptors are involved in apoptoals, and the sequences given can be used in the treatment of cancers, inflections, cardiovascular disorders such as arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms and congenital heart defects, neurodegenerative diseases including Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple sclerosis, arthritis, diabetes, Graves disease, asthma and psoriasis, and to promote angiogenesis and wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQBALCPQVTWSM 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADBAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 DOLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                         Treating graft-versus-host disease, cancer, immunodeficiency or an autoimmune disease comprising administering an antibody to Death Domain Containing Receptor proteins and a second therapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEQRPRGCAAVAAALLIUVLIGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human rheumatoid arthritis associated transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 2323; DB 3; 100.0%; Pred. No. 1.3e-161;
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                                                                                                             Dixit VM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                             Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB97370 standard; protein; 417
                                                                                                                                                                                                                                                          Claim 1; Fig 2; 273pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 417; Conservative
                                                                                                             Gentz RL,
UNIV MICHIGAN
                               NI J.
GENTZ R L.
DILLON P J.
DIXIT V M.
                                                                                                                                           2000-687263/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                              N-PSDB; AAC68777
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 417 AA;
                                                                                                           Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                              (DILL/)
                                 (NIJJ)
                                               (GENT/
                                                                                                           Yu G,
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9903-014939P
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99WO-US028301.
99WO-US028634.
2000WO-US000219.
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99WO-US021090
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                                                                              (first entry)
                                                                                                  Human PRO779 polypeptide
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Matches 417; Conservative
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Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
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Best Local Similarity
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                                                                                                                                                         neuroprotective
                                                                                                                                                                                                   WO200153486-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                          31-AUG-1999;
01-SEP-1999;
15-SEP-1999;
30-NOV-1999;
01-DEC-1999;
01-DEC-1999;
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                             11-FEB-2000;
                                                                                                                                                                                                                                                                                                                                 20-JUL-1999;
26-JUL-1999;
28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marsters SA,
                                                                                                                                                                                                                                                                                                  02-JUN-1999;
22-JUN-1999;
22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe CK,
                                                                              15-JUL-2002
                                                                                                                                                                                                                                                                             11-MAR-1999
11-MAY-1999
                                                                                                                                                                                                                         26-JUL-2001
                                                                                                                                                                                                                                                                  08-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                 17-AUG-1999
                        AAU86139
             RESULT
                                             with rheumatoid arthritis. Certain mutations in the gene can be linked to the disease. The sequences can be used to evaluate disease onset and its possibility and to provide therapy and remedies. The present sequence is a protein described in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the human DR3 gene, which is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALBRMGLDGCVEDLRSRLQRGF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                Genomes, particularly DR3 genomic DNA, participating in rheumatoid arthritis via mutation, useful in evaluating disease onset and its possibility and providing therapy and remedies.
                     Human rheumatoid arthritis associated DR3 gene related protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
                                           Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 2323; DB 5; Length 417; 100.0%; Pred. No. 1.3e-161; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 69-70; 84pp; Japanese.
                                                                                                                                                                           27-MAR-2001; 2001JP-00090546.
30-MAR-2001; 2001JP-00099990.
                                                                                                                                            24-OCT-2001; 2001WO-JP009313
                                                                                                                                                                 24-OCT-2000; 2000JP-00324296
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 417; Conservative
                                                                                                                                                                                                           (NEWI-) NEW IND RES ORG. (SHIO/) SHIOZAWA S.
                                                                                                                                                                                                                                            Shiozawa S, Konishi Y;
                                                                                                                                                                                                                                                                WPI; 2002-417132/44.
N-PSDB; AAL47186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 417 AA;
                                                                                                 WO200234912-A1
                                                                             Homo sapiens.
                                                      therapy
                                                                                                                      02-MAY-2002
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                                                                                                                                                                                                                                                                                                               duman; PRO; benign tumour; malignant tumour; lymphoid malignancy;
leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder;
inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;
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Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 2323; DB 5;
100.0%; Pred. No. 1.3e-161;
iive 0; Mismatches 0;
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Pan J, Pitti RM, Roy MA,
AAU86139 standard; protein; 417 AA
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ABU08252 standard; protein; 417
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                                                                                                    61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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                                                                      CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG
                     MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
MEQRPRGCAAVAAALLLVLLGARAQGGTRS PRCDCAGDFHKKI GLFCCRGCPAGHYLKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APO-3; human; apoptosis; monoclonal antibody; cytostatic; cancer; autoimmune; inflammatory; neurodegenerative disease.
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/note= "Extracellular domain"
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/note= "Transmembrane domain"
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/label= Signal_peptide
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This invention relates to an isolated monoclonal antibody comprising an antigen binding site which binds to an Apo-2 ligand inhibitor (Apo-2LI) polypeptide and an antibody that binds the Apo3 protein. The antibodies of the invention may have cytostatic activity and may act as activators of the invention may have cytostatic activity and may act as activators of the invention may have cytostatic activity and may act as activators or excessive conspotants or the autoimmune/inflammatory effects of Apo-3 resulting from nuclear factor (NF)-kappaB activation or C-Jun-amino-terminal kinase (JNK) activation. The anti-Apo-2 ligand inhibitor is useful in cancer cells and may be used to block excessive apoptosis (for example in neurodegenerative disease), or to block potential autoimmune/FappaB activation or C-Jun-amino-terminal kinase (JNK) activation. The antibody may also be used in diagnostic assays for Apo-2LI or Apo-3, e.g. detecting Apo-2LI or Apo-3 are payression in specific cells, tissues or serum, or for affinity purification of Apo-2LI or Apo-3 from recombinant cells culture or natural sources. The present sequence represents the human Apo3 protein which was used to generate the antibody of the
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                                                                                                    Novel isolated monoclonal antibody useful for activating or stimulating apoptosis in cancer cells, comprises an antigen binding site which binds to an Apo-2 ligand inhibitor polypeptide or to an Apo-3 polypeptide.
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                                                                                                                                                                                                                                                  Claim 1; Fig 4; 48pp; English
   2003-147110/14.
WPI; 2003-147110/
N-PSDB; ABX15842.
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Domain

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61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                   WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                  MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
                                                                                                                                                                                                                                                                                                                          DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                                                                                                                                                                                                                                                                                                                                      101 DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nuclear factor kappa B; NF-kappa B; Alzheimer's disease; AIDS; tumour necrosis factor receptor; acquired immunodeficiency syndrome; Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis; retinitis pigmentosa; cerebellar degeneration; aplastic anaemia; myocardial infarction; stroke; reperfusion injury; toxin-induced liver disease; cancer; lupus; herpes virus infection.
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                                                                             TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG
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                                                                                                                                                                                                                                                                                                                                                                                                                    IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP
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/note= "Death domain. This domain is specifically
claimed in claim 3 of the specification"
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specifically claimed in claim
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/note= "Mature Apo-3 protein"
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG73859 standard; protein; 417 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human foetal heart Apo-3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an new isolated biologically active Apo-2LI or Apo-3 having at least 80 % sequence identity with native sequence Apo-2LI cor Apo-3 appearing as ABU08251 and ABU08251. Also included are a chimaeric molecule comprising the Apo-2LI fused to a hererologous amino acid sequence; a dimer molecule comprising a first Apo-2LI and a second Apo-2LI, an antibody that binds to Apo-2LI or Apo-2LI and a second correctly an antibody that binds to Apo-2LI or Apo-3LI and a second or Apo-3L, a vector comprising the nucleic acid, a host cell comprising the vector, a method of producing Apo-2LI and a non-human (transgenic or knockout) animal that contains cells that express nucleic acid encoding Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3 are involved in apoptosis (programmed cell death) which is implicated in Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3 are involved in apoptosis (programmed cell death) which is implicated in Apo-3 are also varietience and tereal sclerosis, multiple sclerosis, retinitis pigmentosa, aplastic anaemia, cerebellar degeneration, myocardial infarction, reperfusion injury and toxin-induced liver myocardial infarction, reperfusion is located on chromosome 1936.3 Apo-2LI and Apo-3 are also useful for preparing a composition for treating cancer. The present sequence represents Apo-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                          Human, Apo-2 ligand inhibitor, Apo-2LI, Apo-3; apoptosis; AIDS; acquired immunodeficiency syndrome; stroke; Alzheimer's disease; cancer; Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis; retinitis pigmentosa; aplastic anaemia; cerebellar degeneration; myocardial infarction; reperfusion injury; toxin-induced liver disease; chromosome 1q36.3; programmed cell death.
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                                                                                                                                                                                                                                                                           1. .198
/label= Extracellular domain
/note= "This domain is claimed in claim 26"
                                                                                                                                                                                                                                                                                                                                                                                          /note= "This domain is claimed in claim 27"
                                                                                                                                                                                                                                                                                                                                          338. .417
/label= Death_domain
                                                                                                                                                                                                                                                     Location/Qualifiers
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96US-0026943P.
97US-00829270.
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Matches 417; Conservative
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Human Apo-3 protein.
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                                                                                                                                                                                                        Homo sapiens
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This domain is 2 of the specification"

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Towells of apoptosis are associated with diseases such as acquired immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial infarction, stroke, reperfusion injury, and toxin-induced liver disease. The App-3 polypeptide is also useful in non-therapeutic applications such as in quantitative diagnostic assays as control against which samples containing unknown quantities of App-3 may be prepared, in generating antiques, and in competitive-type receptor binding assays. The chimeric cechniques, and in competitive-type receptor binding assays. The chimeric molecule is useful therapeutically to inhibit apoptosis or nuclear factor kappa B (MP-kappa B) induction, or as an immunogen for producing anti-App-3 antibodies. The present sequence represents the polypeptide sequence of the human App-3 protein present in the foetal heart
                                                                                                                                                                                                                                                                                                                    The invention relates to an Apo-3 polypeptide having an extracellular domain (BCD) sequence and a death domain sequence. The Apo-3 polypeptide has been found to stimulate or induce apoptotic activity in mammalian cells. Human Apo-3 exhibits similarities to the tumour necrosis factor receptor (TNFR) family of polypeptides. The invention also relates to a chimeric molecule comprising an extracellular domain sequence comprising residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The Apo-3 polypeptide is useful therapeutically to induce apoptosis in mammalian cells. Decreased levels of apoptosis has been associated with conditions such as cancer, lupus, and herpes virus infection. Increased
                                                                                                                                       Novel isolated Apo-3 polypeptide useful for inducing apoptosis in mammalian cells, for generating antibodies, in affinity purification techniques, and in competitive-type receptor binding assays.
                                                                                                                                                                                                                                                                Claim 1; Fig 8; 52pp; English.
                                                       WPI; 2003-173840/17.
                                                                                      N-PSDB; ABX15464
Ashkenazi AJ;
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Sequence 417 AA;

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                                                                                                                                                       CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                                                                                                                                                                      121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                       MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
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                                                                                                                                                                                                     WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP
                                                                    1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
                                                                                                                                                                                                                                                                       TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG
                                  Gaps
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100.0%; Score 2323; DB 6; Length 417; 100.0%; Pred. No. 1.3e-161; ive 0; Mismatches 0; Indels 0.
                 Best Local Similarity 100.
Matches 417; Conservative
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The invention relates to an isolated Apo-3 polypeptide. The Apo-3 polypeptides are useful for stimulating or inducing apoptotic activity in mammaalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy techniques. The Apo-3 chimeric molecules are useful for inhibiting apoptosis, or as immunogens used in generating antibodies. The antibodies may be used to block excessive apoptosis, for instance in neurodegenerative disease, or to block potential autoimmune/inflammatory effects of Apo-3 resulting from NF-kappas activation. The nucleic acid sequences are useful as diagnostics for tissue-specific kryping, for preparing Apo-3 polypeptides, or for generating transgenic or knockout animals. The transgenic or knockout animals are useful in developing and screening of therapeutically useful reagents. The present sequence represents the amino acid sequence of human Apo-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Apo-3 polypeptides, useful for stimulating or inducing apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo
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                                                                                                                     Human, Apo-3; apoptosis; gene therapy; inflammation; cancer;
neurodegenerative disease; immunosuppresive; tissue typing.
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/label= Extracellular_domain
199. .224
/label= Transmembrane_domain
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/label= Intracellular_domain
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/label= Signal_sequence
                                                                                                                                                                                                                                         5. .417
| Tabel = Mature_Apo-3
                                                                                                                                                                                                                                                                                                                                                                               /label= Death_domain
                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ex vivo gene therapy techniques.
ABU10204 standard; protein; 417 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-2002; 2002US-00112193.
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                                                            (first entry
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Best Local Similarity 100.
Matches 417; Conservative
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                                                                                                                                                                   Homo sapiens
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                                                          11-AUG-2003
                                                                                          Juman Apo-3
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RESULT 13 ABU10204

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Misc-difference 312
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                                                                                                                                           DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARWKEFVRTLGLREAE 360
                                                                                                         417
                                                                                                                                                                                                                                                                                         GENCEPTIN, obesity, lipid partitioning, lipid metabolism; insulin-like activity; free fatty acid oxidation, weight reduction; annonectic; antilipaemic; antiarteriosolerotic; cardiant; antidiabetic; hypotensive; ophthalmological; neuroprotective; nephrotropic; obesity-related disease; insulin resistance; atherosoclerosis; atheromatous disease; heart disease; cardiac insufficiency; ocoronary insulficiency; high blood pressure; hypertension; stroke; syndrome X; diabetes mellitus; hyperlipidaemia; hyperuricaemia; diabetic complication; microangiopathic lesion; ocular lesion; retinopathy; neuropathy; renal lesion.
                                                                                                                                                                           TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG
                               WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP
                                                                                                                                                                  I EAVEVEIGR FRDOOYEMLKRWROOOPAGLGAVYAALERWGLDGCVEDLRSRLORGP
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200. .222
/label = transmembrane_domain
223. .417
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116. .163
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/note= "Cys rich region"
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164. 192
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                                                                                                                                                                                                                                                                            Human GENCEPTIN protein SEQ ID NO:2.
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/label= GENCEPTIN
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'label= signal
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/label -
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The present invention describes the use of an agonist or antagonist of GENCEPTIN activity for preventing or treating obesity. Also described is a method of screening for GENCEPTIN activity. Also described is a method of screening for GENCEPTIN set since fatty acid oxidation, and useful partitioning, lipid metabolism, insulin-like activity, free fatty acid oxidation, and weight reduction. GENCEPTIN has anorectic, antilipaemic, ophthalmological, neuroprotective and nephrotropic activities. GENCEPTIN can be used for treating or preventing obesity-related disease or disorders, e.g. obesity, insulin resistance, atherosalerosis, atheromatous disease, heart disease (e.g. cardiac insufficiency, thigh blood pressure), hypertension, stroke, syndrome X, diabetes mellitus (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic compilications, e.g. microangiopathic lesions, ocular lesions, retinopathy, neuropathy and renal lesions. The present sequence represents human GENCEPTIN, which is given in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New use of Genceptin agonists or antagonists for treating or preventing obesity-related diseases or disorders.
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                                                                     Leu"
   or Arg
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/note= "polymorphic amino acid Ala
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                                                                                                                                   /note= "polymorphic amino acid Arg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Briggs K;
                                                                                                                                                                                                                                                                                                                                    31-JUL-2002; 2002WO-IB003418.
                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2001; 2001US-0309818P.
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417; Conservative
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                                  Misc-difference 370
                                                                                                    Misc-difference 381
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                                                                                                                                                                                                                                                                                                                                                                  'note= "Specifically claimed in claim 4. Residues 1-181
                                                                                                                                                          human; Apo-2 ligand inhibitor; Apo-2LI; apoptosis; NF-kappaB; JNK; c-Jun N-terminal kinase; necrosis factor kappa B; chimeric molecule; tissue-specific typing; Apo-3; transgenic; affinity purification; competitive-type receptor binding assay.
       New isolated biologically active Apo-2LI or Apo-3 used to induce apoptosis in mammalian cells.
                                                                                                                                                                                                                                                                                                                                             16. 163
| label = Cysteine-rich_domain_3
                                                                                                                                                                                                                                                                                                                   'label= Cysteine-rich_domain_1
                                                                                                                                                                                                                                                                                                                                     Cysteine-rich_domain_2

    198
    Iabel= Extracellular_domain

                                                                                                                                                                                                                                                                                              of Apo-3 represent Apo2LI"
                                                                                                                                                                                                                                                                                                                                                                                                            338. .417
/label= Death_domain
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                            ABG73824 standard; protein; 417
                                                                                                                                        Human apoptotic protein, Apo-3.
                                                                                                                                                                                                                                                                 |. .181
|abel= Apo-2LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 22; Fig 4; 44pp; English
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96US-00710802.
97US-00828683.
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/label= C
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23-SEP-1996;
31-MAR-1997;
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                                                                                                 ABG73824;
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                                                         RESULT 15
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apoptosis in vivo or ex vivo. Nucleic acid sequences encoding the Apo-3 or Apo-2LI may be used as a diagnostic for tissue-specific typing. The isolated Apo-2LI may be used in quantitative diagnostic assays as a control against which samples containing unknown quantities of Apo-3LI may be prepared. Apo-3 preparations are also useful in craffinity purification techniques, and in competitive-type receptor. If it is affinity purification techniques, and in competitive-type receptor. It is affinity purification techniques, and in competitive-type receptor. It is affinity purification techniques, and in competitive-type receptor. It is affinity purification techniques, and in competitive-type receptor. It is affinity purification techniques, and in competitive-type receptor. It is affinity purification are apolitically acid forms of the Apo-3, e.g. Apo-3-1gG chimeric. The Apo-3 exists antibodies. Nucleic acids which encode Apo-3 or its modified forms can also be used to generate either transgenic animals or knock out animals. e.g. mouse or cat, which, in turn, are useful in the development and screening of therapeutically useful in reagents. The Apo-3 polypeptide stimulates or induces apoptotic activity in mammalian cells. The present sequence represents the human apoptotic protein, Apo-3 residues 1-181 of Apo3 creptored or soluble form of Apo3
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Matches 417; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-314-889-4
US-10-01-889-4
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US-10-012-793-6
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12 2223 100.0 417 14 US-10-211-884-24 Sequence 24, Appli 2223 100.0 417 15 US-10-310-793-4 Sequence 24, Appli 16 US-10-310-793-4 Sequence 24, Appli 16 US-10-648-862-5 Sequence 3, Appli 17 15 US-10-648-862-5 Sequence 5, Appli 2223 100.0 417 16 US-10-744-379-2 Sequence 5, Appli 2223 100.0 417 16 US-10-744-379-5 Sequence 5, Appli 2223 100.0 813 14 US-10-226-296-5 Sequence 5, Appli 2223 100.0 813 14 US-10-226-348-5 Sequence 5, Appli 223 100.0 813 14 US-10-226-348-5 Sequence 5, Appli 223 100.0 813 14 US-10-26-348-5 Sequence 5, Appli 223 100.0 813 16 US-10-648-786-5 Sequence 5, Appli 223 100.0 813 16 US-10-648-786-5 Sequence 5, Appli 223 100.0 813 16 US-10-648-786-5 Sequence 5, Appli 224 2267 97.6 428 10 US-10-648-786-5 Sequence 2, Appli 225 2267 97.6 428 10 US-10-913-294-2 Sequence 2, Appli 226 1404 60.4 411 16 US-10-189-189-2 Sequence 2, Appli 226 1404 60.4 411 16 US-10-189-189-2 Sequence 1, Appli 226 1601 45.2 181 9 US-0-931-244-1 Sequence 1, Appli 226 1601 45.2 181 13 US-10-112-193-1 Sequence 1, Appli 236 161 45.2 181 13 US-10-112-193-1 Sequence 1, Appli 236 161 45.2 181 13 US-10-112-193-1 Sequence 24, Appli 236 161 4 45.4 15 US-10-22-2-24-5 Sequence 15, Appli 237 16.4 45.4 15 US-10-242-2 Sequence 15, Appli 238 181 16.4 45.4 15 US-10-22-2-2 Sequence 15, Appli 239 181 16.4 45.1 181 US-10-22-3-15 Sequence 15, Appli 239 181 16.4 45.1 181 US-10-22-3-15 Sequence 15, Appli 41 180.5 US-0-999-222-15 Sequence 15, Appli 41 180.5 US-0-999-222-15 Sequence 15, Appli 242 180.5 US-0-999-222-15 Sequ
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ALIGNMENTS

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US-09-313-956.

JS-09-133-956.

JS-09-133-956.

Patent No. US20020009773A1

GENERAL INFORMATION:

APPLICANT: Ni, Jian

APPLICANT: Dixit, Vistva

APPLICANT: Dixit, Vistva

APPLICANT: Dixit, Vistva

APPLICANT: Dixit, Vistva

APPLICANT: Dillon, Patrick J.

TITLE OF INVENTION:

APPLICANT: Dillon, Patrick J.

TITLE OF INVENTION:

APPLICANT: Dillon, Patrick J.

TITLE OF INVENTION:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.C.

STRAFE: DC

CONTRY: USA

ZIP: Z0005-3934

COUNTRY: USA

ZIP: Z0005-3934

COUNTRY: USA

ZIP: PLING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin PC-DOS/MS-DOS

SOFTWARE: PATENTINON DATA:

APPLICATION NUMBER: NO. US20020009773A1 Yet Assigned

FILING DATE: 06-FEB-1997

PRIOR APPLICATION DATA:
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COUNTRY: USA
                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                              LENGTH: 417
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Patent No. US20020072091A1
GENERAL INFORMATION:
APPLICANT: N. Jan
APPLICANT: Yu, Guo-liang
APPLICANT: Yu, Guo-liang
APPLICANT: Yu, Guo-liang
APPLICANT: Resen, Craig A.
TITLE OF INVENTION: Death Domain Containing Receptor 5
FILE REFERENCE: 1488.1310006
CURRENT APPLICATION NUMBER: 08/09/874,138
CURRENT FILING DATE: 2001-06-06
PRIOR FILING DATE: 2000-05-04
PRIOR PLICATION NUMBER: 60/148,939
PRIOR PLICATION NUMBER: 60/148,939
PRIOR PLICATION NUMBER: 60/13,238
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECHONE: 202-371-2600
TELECHONE: 202-371-2600
TELECHONE: 202-371-2600
TELEPRAXICON FOR SEC 1D NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 LENGTH: 417 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-09-333-966-4
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Sequence 6, Application US/09993234

Patent No. US20020146768A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

BUDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winheatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/993,234
FILING DATE: 19-No. US20020146768A1-2001
CLASSIFICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 2323; DB 9;
100.0%; Pred. No. 5.3e-163;
ive 0; Mismatches 0;
PRIOR FILING DATE: 1999-05-04

PRIOR PLING DATE: 1998-03-17

PRIOR PTLING DATE: 1998-03-17

PRIOR APPLICATION NUMBER: 60/054,021

PRIOR PLING DATE: 1999-7-07-29

PRIOR APPLICATION NUMBER: 60/040,846

PRIOR PLING DATE: 1997-03-17

NUMBER: 0F SEQ ID NOS: 14

SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 417; Conservative
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Indels
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              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,889
                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INPORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
                                                                                                         PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/815,469
FILING DATE:
PRICR APPLICATION NUMBER: 06/028,711
APPLICATION NUMBER: US 60/028,711
FILING BATE: 17-007-1996
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, ETIC K.
REGISTRATION NUMBER: 36,688
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/10005842 Publication No. US20020098550A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ni, Jian
Gentz, Reiner
Yu, Guo-Liang
Su, Jeffrey
Rosen, Craig A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 417 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-005-842-5
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| Publication No. US20030077694A1
| GENERAL INFORMATION:
| FAPLICANT: Vision | APPLICANT: Dixit, Vision | APPLICANT: Dixit, Vision | APPLICANT: Dixit, Reiner L. | APPLICANT: Dillon, Retrick J. | TITLE OF INVENTION: Death Domain Containing Receptors | NUMBER OF SEQUENCES: | CORRESPONDENCE ADDRESS: | ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 2323; DB 9;
100.0%; Pred. No. 5.3e-163;
rative 0; Mismatches 0;
          ATTORNEY AGENT INFORMATION:
NAME: MARSTANDON INFORMATION:
RAGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELEPHONE: 415/225-981
TELEFAX: 916/31-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS;
APPLICATION NUMBER: 08/828,683
                                                                                                                                                                                                                                                                         TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                    LENGTH: 417 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPANY. ....ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
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Best Local Similarity 100.0
Matches 417; Conservative
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61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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                                                                                                                                                                                                      1 MEQRIPRGCAAVAAALLIVLIGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW
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                                                                                                                                                    1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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Length 417;
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240

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US-10-081-280-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
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                                                                                                 STATE: ND
COUNTRY: US
ZIP: 20850
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTE: ISM PC compatible
COMPUTE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/005,842
FILING DATE: 07-Dec-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION: <UNKNOWN>
PRIOR APPLICATION: <UNKNOWN>
TITLE OF INVENTION: Death Domain Containing Receptor
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/042,583
FILING DATE: «Uhknown»
APPLICATION NUMBER: US 60/040,846
FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
             NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Scier
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: HOOVEY, KENLEY
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PFI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3013098504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 417 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 3013098439
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CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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Sequence 6, Application US/10081280
Publication No. US20020165157A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech)

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/081,280

FILING DATE: 21-Feb-2002

CLASSIFCATION: <UNKnown>
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APPLICATION NUMBER: US/08/829,270
FILING DATE: 31.Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: MARESCHAIG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                    ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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TYPE: Amino Acid
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Matches 417; Conservative
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CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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                                                                                   361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGF 417
                                                                                                             1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,193
FILING DATE: 28-Mar-2002
CLASSIFICATION ATMANS: 08/928,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 08/928,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
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100.0%; Pred. No. 5.3e-163;
tive 0; Mismatches 0;
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Sequence 10, Application US/10112193
Sequence 10, Application US/10112193
Sequence 10, Sequence 10, Sequence 10, Publication No. US20030004313A1
GENERAL INFORMATION:
TITLE OF INVENTION: App-3 POLYPEPTIDE
NUMBER OF ERQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
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SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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STATE: California
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Best Local Similarity 100.
Matches 417; Conservative
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  361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
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                                                                           Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wilpatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION **CURRION**
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
FILING DATE: 23-Sep-1996
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REGISTRATION NUMBER: 35,600
REPERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
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US-10-112-793-6
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Best Local
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CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                     361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGF 417
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                                                                                                                                                                                               Sequence 4, Application US/10189189
| Sequence 4, Application US/10189189
| Publication No. US20030170203A1
| GENERAL INFORMATION:
| APPLICANT: Ni, Jian
| APPLICANT: Ni, Jian
| APPLICANT: Dixit, Vishva
| FILE REPERENCE: 1480: 0310, 189
| FILE REPERENCE: 1480: 0314, 314
| PRIOR PILING DATE: 2001-07-06
| PRIOR PILING DATE: 2001-06-10
| PRIOR PILING DATE: 1999-05-28
| PRIOR PILING DATE: 1999-05-28
| PRIOR PILING DATE: 1999-06-28
| PRIOR PILING DATE: 1999-06-26
| PRIOR PILING DATE: 1999-06-26
| PRIOR PILING DATE: 1999-06-26
| PRIOR PILING DATE: 1996-03-11
| PRIOR PILING DATE: 1996-03-12
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100.0%; Pred. No. 5.3e-163;
Mismatches 0;
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Best Local Similarity 100.
Matches 417; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4
FILE REPERENCE: 1488.130005
CURRENT APPLICATION NUMBER: 005.65,918
FRICH APPLICATION NUMBER: 005.65,918
FRICH APPLICATION NUMBER: US 60/132,922
FRICH RILING DATE: 2090-05-06
FRICH APPLICATION NUMBER: US 60/013,895
FRICH FILING DATE: 1999-01-27
FRICH APPLICATION NUMBER: US 60/037,829
FRICH FILING DATE: 1997-01-28
FRICH APPLICATION NUMBER: US 60/035,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/10175902
Publication No. US20030108516A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 417; Conservative
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FILE REPRENCE PESSITIANI
FILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
FILE REPRENCES: PESSITRACI
CURRENT APPLICATION NUMBER: US/10/211,884
CURRENT FILING DATE: 1996-09-02
FRIOM FILING DATE: 1996-09-13
FRIOM FILING DATE: 1996-09-13
FRIOM FILING DATE: 1997-07-17
FRIOM FILING DATE: 1997-07-17
FRIOM FILING DATE: 1997-07-17
FRIOM FILING DATE: 1997-09-19
FRIOM FILING DATE: 1997-09-19
FRIOM FILING DATE: 1997-01-10
FRIOM FILING DATE: 1997-10-10
FRIOM FILING DATE: 1997-10-24
FRIOM FILING DATE: 1997-10-24
FRIOM FILING DATE: 1997-10-24
FRIOM FILING DATE: 1997-11-24
                                                                                                                 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
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                                                                                                                                                                                                                                                                  181 TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
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Publication No. US20030175900A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan, James
Pitti, Robert M.
Roy, Margaret Ann
Smith, Victoria
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Watanabe, Colin K.
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Marsters, Scot A
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Best Local Similarity 100.
Matches 417; Conservative
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ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: 60/014699
PRIOR FILING DATE: 1996-04-01
PRIOR PLILING DATE: 1996-04-01
PRIOR PLILING DATE: 1996-03-33
PRIOR FILING DATE: 1997-07-17
PRIOR PLILING DATE: 1997-07-17
PRIOR PPLICATION NUMBER: 60/059352
PRIOR PPLICATION NUMBER: 60/059352
PRIOR PPLICATION NUMBER: 60/062037
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-17
PRIOR PLILING DATE: 1997-10-24
PRIOR PPLICATION NUMBER: 60/063045
PRIOR PLILING DATE: 1997-10-24
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APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR PILE REPERRICE: P2931R1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP
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                                                                                                                                                                                                                                                           Sequence 24, Application US/10210951
Publication No. US20030170228A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan, James
Pitti, Robert M.
Roy, Margaret Ann
Smith, Victoria
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Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 100.
Matches 417; Conservative
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US-10-210-951-24
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Qy 1 MEORPRGCAAVAAALLLVLIGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP 60 Db 1 MEORPRGCAAVAAALLLVLIGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP 60 C 61 CTEPCGASTCLVCPQDTFLAMENHHVSECARCACDEQASQVALENCGAVADTRCGCKPG 120 CY 121 WFVECQYSCOCSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180 Db 121 WFVECQYSCOCSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180 CY 121 WFVECQYSGOCSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180 CY 121 WFVECQYSGOCYSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180 CY 121 WFVECQYSGOCYSSSPFYCQPCLAGGLYDVBLATTYTYRHCWPHKPLVTADEAG 240 CY 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQYTWSW 300 CY 301 DQLPSRALGPAAPTLLSPESPAGSPAWILQPGPQLYDVMDAVPARRWKEFVRTLGIRRAE 360 CY 301 DQLPSRALGPAAPTLSPESPAGSPAMILQPGPQLYDVMDAVPARRWKEFVRTLGIRRAE 360	Oy 351 IEAVEVEIGREPDOOYEMLKRWROOPPAGIGAVYAALERKGLORGF 417 RESULT 14 US-10-211-858-24 1 Sequence 24, Application US/10211858 1 PADLICANT: Abhenazi Avi J. 2 APPLICANT: Gadard Audrey 2 APPLICANT: Gadard Audrey 3 APPLICANT: Gadard Audrey 3 APPLICANT: Gadard Audrey 4 APPLICANT: Gadard Audrey 5 APPLICANT: Gadard Audrey 6 APPLICANT: Gadard Audrey 7 APPLICANT: Gadard Audrey 7 APPLICANT: Gadard Audrey 8 APPLICANT: Gadard Audrey 8 APPLICANT: Gadard Audrey 8 APPLICANT: Gadard Audrey 9 APPLICANT: Gadard Audrey 9 APPLICANT: Gadard Audrey 1 APPLICANT: Gadard 1 APPLICANT: Gadard 1 APPLICANT: Gadard 1 APPLICANT: Gadard 1 APPLICANT:	PRIOR Remain NUMBER
0y 61 CTEPCGNSTCLVCPODTFLAWENHHNSECARCOACDEOASQVALENCSAVADTRCGCKPG 120 Db 61 CTEPCGNSTCLVCPODTFLAWENHHNSECARCOACDEOASQVALENCSAVADTRCGCKPG 120 Oy 121 WFVECQVSQCVSSSPPYCQPCLDCCALHRHTRLCSRRDTDCGTCLPGFYEHGDGCVSCP 180 Db 121 WFVECQVSQCVSSSPPYCQPCLDCGALHRHTRLCSRRDTDCGTCLPGFYEHGDGCVSCP 180 Oy 181 TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240 Db 181 TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240 OY 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300 C41 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300 C42 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300 C43 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300 C44 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETGEALCPQVTWSW 300 C45 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETGEALCPQVTWSW 300 C47 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETGEALCPQVTWSW 300 C48 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETGERAE 360 C67 MEALTPPPATHLSPLDSAMMLQPGPQLYDVMDAVPARRWEFVRTLGIREAE 360 C67 MEALTPPPATHLSPLDSAMMLQPGPQLYDVMDAVPARRWEFVRTLGIREAE 360 C67 MEALTPPPATHLSPLDQVEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417 C67 MEALTPPPATHLSPLDQVEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417 C67 MEALTPPPATHLSPLDQVEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417 C67 MEALTPPATHLSPLDQVEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417 C67 MEALTPPATHLSPLDQVEMLKRWRQQQPATHCHANGN MANDAVARRAMKEFVRTLGIREAE 360 C67 MEALTPPATHLSPLDQVEMLKRWRQQQPATHCHANGN MANDAVARRAMKEFVRTLGIREAE 360 C67 MEALTPPATHLSPLDQVEMLKRWRQQQAVARRAMKEFVRTLGIREAE 360 C68 MEALTPPATHLSPLDQVEMLKRWRQQQAVARRAMKEFVRTLGI	4 Application US/10310793 NRMATION: Vu, Guo-Liang Noi. Jian Wel, Ping VENTION: Relating To Huma NEE: PF573 LICATION NUMBER: US/10/310 LING DATE: 2002-12-06 CATION NUMBER: 10/226,294 G DATE: 2001-08-24 CATION NUMBER: 60/314,381 G DATE: 2001-08-24 CATION NUMBER: 60/216,879 G DATE: 2001-08-24 CATION NUMBER: 60/216,879 G DATE: 2001-08-24 CATION NUMBER: 60/216,879 G DATE: 2000-07-07 CATION NUMBER: 60/134,067 G DATE: 2000-04-27 CATION NUMBER: 60/134,067 G DATE: 2000-04-27 CATION NUMBER: 60/134,067 G DATE: 2000-02-08 CATION NUMBER: 60/134,067 G DATE: 1999-05-13 TION NUMBER: 60/132,27 ALON NUMBER: 60/134,067 G DATE: 1999-05-13 TION NUMBER: 60/134,067 G DATE: 1999-05-13 TION NUMBER: 60/134,067 ALON NUMBER: 60/134,067 G DATE: 1999-05-13 TION NUMBER: 60/134,067 ALON NUMBER: 60/134,067 G DATE: 1999-05-13 TION NUMBER: 60/134,067 ALON NUMBER: 60/134,067 G DATE: 1999-05-13 TION NUMBER: 60/134,067 ALON NUMBER:	

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TITLE OF INVENTION: chronic rheumatoid arthritis

TITLE OF INVENTION: chronic rheumatoid arthritis

FILE REFERENCE: TLOSP-2

CURRENT APPLICATION NUMBER: US/10/415,247

CURRENT FILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-10-24

PRIOR FILING DATE: 2001-3-27

PRIOR FILING DATE: 2001-3-27

PRIOR FILING DATE: 2001-3-27

PRIOR FILING DATE: 2001-3-27

SPRIOR FILING DATE: 2001-3-27

SPRIOR FILING DATE: 2001-3-27

SPRIOR FILING DATE: 2001-3-30

NUMBER OF SEQ ID NOS: 21

SSQTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                   121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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                                                                                                                                                                                                   1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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                                                                                                                  / Match 100.0%; Score 2323; DB 15; Length 417; Local Similarity 100.0%; Pred. No. 5.3e-163; Nes 417; Conservative 0; Mismatches 0; Indels 0;
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Publication No. US20040013655A1
GENERAL INFORMATION:
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Matches 417; Conservative
                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-858-24
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US-10-415-247-3
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SEQ ID NO 24
LENGTH: 41
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WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                     CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                                                                          WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
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1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP 60
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                                              CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG
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Search completed: June 27, 2005, 13:56:23 Job time : 163 secs

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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- protein search, using sw model OM protein Run on:

June 27, 2005, 13:52:39 ; Search time 43 Seconds (without alignments) 436.332 Million cell updates/sec

US-10-081-280-6_COPY_1_195 Title: Perfect score:

1 MEQRPRGCAAVAAALLLVLL.........CVSCPTSTLGSCPERCAAVC 195 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

99046 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 195 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Fas-Delta-(4,7) pr metallothionein-2 ultra-high-sulfur finger protein zfo cysteine-rich hair protein B0238.12 [ultra-high-sulfur high-cysteine chor high-sulfur kerati ultra high-sulfur high cysteine chor trophozoite surfac finger protein (cl cellular nucleic a cellular nucleic a cellular nucleic a keratin high-sulfu high-sulfur wool m hypothetical prote keratin high-sulfu zinc finger protei cellular nucleic a high sulfur protei hypothetical prote hair keratin cyste ferredoxin-type pr cellular nucleic a keratin KAP5.4 - s Description SUMMARIES S50911 A36686 S70007 I46489 H89044 A55499 146412 AG0369 148298 JC6547 T20467 S60314 S06570 A45910 A23219 S37649 S18946 B21761 PC1294 149259 **CRGT3M** r24272 В % Query Match Length E 170 170 191 191 171 188 193 151 168 89.5 89.5 89.5 89.5 88 84.5 84.5 84.5 84 83.5 83.5 82.5 82.5 111 107 103.5 96.5 96 94.5 94 103 Score Result No.

hypothetical prote

agglutinin isolect	hypothetical prote	Putative electron	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	iron-sulfur cluste	high-sulfur kerati	hypothetical prote	epithelial cell gl	arginine-vasotocin	probable iron-sulp	probable metalloth	keratin high-sulfu	high-sulfur wool m
A28401	F65072	G65156	T25185	T15610	F86032	H91185	B82430	837650	T20463	D37057	S14480	AB0361	E833.78	KRSHHC	147111
N	N	N	N	~	~	N	н	N	N	7	~	N	~	Н	N
186	163	157	160	135	157	157	168	177	132	92	191	189	79	152	152
7.2	7.1	7.1	7.1	7.0	7.0	7.0	7.0	7.0	7.0	6.9	6.9	6.9	6.9	6.9	6.9
81 7.2		80 7.1	80 7.1							78.5 6.9			78 6.9	78 6.9	78 6.9

ALIGNMENTS

 C; Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004 C; Accession: A45910 C; Accession: A45910 C; Accession: A45910 C; Accession: A5910 J. Divest. Dermatol. 92, 263-266, 1989 A; Title: An ultra-high sulfur keratin gene is expressed specifically during hair growth. A; Reference number: A45910; MUID:89140394; PMID:2465353 A; Accession: A45910 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-186 < ACCNS A; Accession: A45910 A; Cross-references: UNIPROT:Q64526; GB:M27685; NID:9341749; PIDN:AAA81560.1; PID:91066818 C; Superfamily: ultra-high-sulfur keratin
Query Match Best Local Similarity 24.8%; Pred. No. 0.18; Matches 39; Conservative 15; Mismatches 67; Indels 36; Gaps 8;
QY 47 CCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQAS 100
QY 101 QVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRR 158
Qy 159 DTDCGTCLPGFYEHGDGCVSCPTSTLGSCPERCAAVC 195
RESULT 2 A2319 high-cysteine chorion protein B 13 - silkworm C;Species: Bombyx mori (silkworm) C;Species: Bombyx mori (silkworm) C;Species: Bombyx mori (silkworm) C;Accession: A2319 R;Rodakis, G.C.; Lecanidou, R.; Bickbush, T.H. J. Mol. Evol. 20, 255-273, 1984 A;Title: Diversity in a chorion multigene family created by tandem duplications and a put A;Reference number: A92960; MUID:85083111; PMID:6439880 A;Accession: A2319 A;Molecule type: DNA A;Residues: 1-178 <rod> A;Accession: A2319 A;Rote: the authors translated the codon CTG for residue 48 as Val and GAG for residue 6: C;Genetics: A;Introns: 17/3 C;Superfamily: chorion class A protein pc292</rod>

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Rilatrou, K.; Tsitilou, S.G.; Kafatos, F.C.
Proc. Natl. Acad. Sci. U.S.A. 81, 4452-4456, 1984
A;Title: DNA sequence transfer between two high-cysteine chorion gene families in the sil
A;Reference number: A21761; MUID:84272653; PMID:6589605
A;Accession: B21761
A;Cross-references: UNIPROT:Q14564; EMBL:X63755; NID:g32471; PIDN:CAA45283.1; PID:g32472 R;MacKinnon, P.J.; Powell, B.C.; Rogers, G.E. Cell Biol. 111, 2587-2600, 1990 A;Title: Structure and expression of genes for a class of cysteine-rich proteins of the cA;Reference number: A36686; MUID:91115951; PMID:1703541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 NSTCLVC------PQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 EQASQVALENCSAVADTRCG-C--KPGWFVECQVSQCVSSSPFYC----QPCLDCGALH 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 PVCCCVPACSCSSCGKRGCGSCGGSKGGCGSCGCSQCSCCKPCCCSSGCGSSCCQCSC-- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 CCRGCPAGHYLKAPCTEPCG--NSTCLVCPQDTFLAWENHHNSECARCQ-----ACD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CC-GCSGG-----CGSSCGGCDSSCGSC-----GSGCRGCGPSCCAPVCCCK 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 RHTRLLCSRRDTDCGTCLPGFYEHGDG---CVS-----CPTSTLGS--CPERCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ckpycsockpccsssdrdssccokpccssdcdssccdsscdsscco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B21761
high cysteine chorion B 12 protein precursor - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Jan-2000
C;Accession: B21761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 VAAALLL----VLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 GCGCGCCENFRVCSNSAAPTGLSICSENRYKGDVC---VCGEVPFLGTADVCGNMCSSGC
                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-39,'Y',41-169 <MAC>
A;Cross-references: GB:X55293; NID:g34078; PIDN:CAA39005.1; PID:g34079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 8.6%; Score 97; DB 2; Length 143; 1 Similarity 21.5%; Pred. No. 1.6; 43; Conservative 14; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.1%; Score 103; DB:
25.3%; Pred. No. 0.63;
tive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F,108-117/Region: Cys-rich decapebtide repeat
F;118-126/Region: Ser-rich nonapeptide repeat
F;127-136/Region: Cys-rich decapeptide repeat
F;137-145/Region: Cys-rich nonapeptide repeat
F;146-155/Region: Cys-rich decapeptide repeat
F;156-165/Region: Cys-rich decapeptide repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-13 < LATA <
C;Superfamily: chorion class A protein pc292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;98-107/Region: Cys-rich decapeptide repeat
                                                                                                                                                                                                                                                                                                                                           A,Map position: 11q13-11q13
C,Superfamily: ultra-high-sulfur keratin
C,Superfamily: ultra-high-sulfur keratin
C,Superfamily: ultra-high-sulfur keratin
F,7-15/Region: Ser-rich nonapeptide repeat
F,59-68/Region: Gly-rich decapeptide repeat
F,79-88/Region: Cys-rich decapeptide repeat
F,79-88/Region: Ser-rich nonapeptide repeat
F,89-97/Region: Ser-rich nonapeptide repeat
                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:125257; OMIM:148021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 45; Conserv
                                                                                                                                                    A; Accession: B36686
                                                                                                                                                                                                                                                                                            A; Gene: GDB: KRN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
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                                                                                                                                                                                                                                                                 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
837649
high selfur keratin - human
c;Species: Homo sapiens (man)
c;Species: Homo sapiens (man)
c;Accession: 837649
R;Zhumabaeva, B.D.; Gening, L.V.; Gazaryan, K.G.
Mol. Biol. 26, 550-555, 1992
A;Title: Cioning and structural characterization of human hair sulfur-rich keratin genes
A;Reference number: 837649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q07628; EMBL:X63338; NID:g311881; PIDN:CAA44938.1; PID:g3118
C;Superfamily: keratin high-sulfur matrix protein IIIA
                                                              12;
                                                                                                                                                                                                                              67 NSTCL----VCPQDTFLAWENHHNSECARC-----QACDEQASQ-----VALEN 106
                                                                                                                                                                                                                                                                    ECARCQACDEQASQVA---LENCS-AVADTRCGCKPGWFVECQVSQC------ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 -----VSSSPFYCQP----CL-DCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDG 175
                                                                                                                                                                                                                                                                                                                                                                                                       -----CGG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 QEGSSGAVSTRIRWCRPDCRVEGTCLPPCCVVSCHTPTCCQLHHAEASCCRPSYC--GQS 161
                                                                                                                                                                                                                                                                                                                                              CSAVADT -- RCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGT 164
                                                                                                                      99
                                                                                                                                                                           43
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Ultra high-sulfur keratin 1 - human

Ultra high-sulfur keratin 1 - human

U.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C.Accession: S18946; B3666

C.Accession: S18946; Banecke, D.

Submitted to the EMBL Data Library, December 1991

A.Description: Nucleotide sequence of a Human high-sulphur keratin cDNA.

A.Reference number: S18946

A.Moccession: S18946
                                                                                                                11 VAAALLL----VLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCG
                                                                                                                                                    31 PRCDCAGDFHKKIGLFCCR-GCPAGHYLKAPCTEP--CGNSTCLVCPQDTFLAWENHHNS
                                                              72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 175;
     DB 2; Length 178;
                                                        77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       104 CVGITQSCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
9.5%; Score 107; DB 2
23.2%; Pred. No. 0.33;
iive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLPGFYEHGDGCVSCPTSTLGSCPERCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GCGCGGC-----GGC--GCCGGC 165
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Local Similarity 22.5%; Pred. No. 0.6;
Ne 45; Conservative 15; Mismatches
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                                                        49; Conservative
                       Best Local Similarity
Matches 49; Conserv
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A;Residues: 1-175 <ZHU>
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     Query Match
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HGDG 175 QY 44 GLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWBNHHNSECARCQACDE 97	RESULT 8 S50911 metallothionein-2 - Tetrahymena piqmentosa	C;Species: Tetrahymena pigmentosa C;Date: 119-541-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 C;Date: 11-5-Uul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 C;Accession: 850911 R;Piccinni, E.; Staudenmann, W.; Albergoni, V.; de Gabrieli, R.; James, P. R;Piccinni, E.; Staudenmann, W.; Albergoni, V.; de Gabrieli, R.; James, P. A;Title: Purification and primary structure of metallothioneins induced by cadmium in the A;Reference number: 850911 A;Accession: 850911 A;Accession: S50911 A;Accession: S50911 A;Accession: S50911 A;Accession: S50911 A;Accession: S60911 A;Accessio	A; Genetic code: SGC5 Query Match Best Local Similarity 34.3%; Pred. No. 1.9 Matches 23; Conservative 8; Mismatches Qy 33 CDCAGDFHKKIGLFCCRGCPAGHYLKAPC	9; Db 40	56 164		R;MacKinnon, P.J.; Powell, B.C.; Rogers, G.B. J. Cell Biol. 111, 2587-2600, 1990 A;Title: Structure and expression of genes for a class of cysteine-rich proteins of the A;Reference number: A36686; MUID:91115951; PMID:1703541 A;Accession: A36686 A;Status: preliminary	· · · -	eral blood mononuc Query Match 8.3%; Score 94; DB 2; Length 182; Best Local Similarity 22.8%; Pred. No. 3; Matches 45; Conservative 6; Mismatches 74; Indels 72; Gaps 13;	Qy 7 GCAAVAAALLIVILGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTE 63	Qy 64 PCGNSTCLVCPQDTFLAWENHHNSECARCDACDEQASQVALENCSAVADTRCGCKPGW 121	Oy 122 FVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVS 178	
QY 116 GCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDG	Qy 176 CVSCPTSTLGSCPERCAAVC 195 Db 125 CGGCGCCGCSCGRSC 139	RESULT 6 PC1294 trophozoite surface antigen - Giardia lamblia (strain Adelaide-1) (fragment C;Species: Glardia lamblia C;Species: Glardia lamblia C;Bacession: PC1294 R;EY, P.L.; Mayrhofer, G. R;EY, P.L.; Mayrhofer, G. Acnee 129, 257-262, 1993 A,Title: Two genes encoding homologous 70-kDa surface proteins are present 'A;Reference number: PC1294; MUD:93314970; PMID:8325510 A,Mocession: PC1294 A,Molecule type: DNA	lues: 1-141 <eyp> s-references: UNIPROT:P21849; GB:M97488 s-references: UNIPROT:P21849; GB:M97488 rtsa: tsa: ords: surface antigen Match Match</eyp>	Heer Local Similarity 27.2%; Pred. No. 1.7; Matches 41; Conservative 10; Mismatches 65; Indels 35; 66 GNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADT	3 GASYCSECATTT 117 CKPGWFVEC	Db 57 CYETVKYPGKTVCISAPNGGICQKAADGYKLDSGTLTVCSEGCKECTSSTDCTT QY 165 CLPGFYEHGDGCVSCPTSTLGSCPERCAA 193	RESULT 7 S58662 Fas-Delta-(4,7) protein - human C.Soecies: Homo sapiens (man)	C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004 C;Accession: SS86652; SS7566 R;Liu, C; Cheng, J; Mountz, J.D. Biochem. J. 310, 957-963, 1995	A;Title: Differential expression of human Fas mRNA species upon peripheral bloo A;Reference number: \$58662; MUID:96013198; PMID:7575433 A;Accession: \$58662; MUID:96013198; PMID:7575433 A;Accession: \$58662 A;A;Accession: \$58662 A;A;Accession: \$78662 A;A;Accession: \$78662 A;A;A;A;A;A;A;A;A;A;A;A;A;A;A;A;A;A;A;	;	aubmitted to the EMBL Data Library, June 1995 A;Reference number: 857565 A;Accession: 857566 A;Status: preliminary	A;Molecule type: mkNA A;Residues: 1-132 <sch> A;Cross-references: EMBL:X89101; NID:g887457; PID:g887458 C;Keywords: alternative splicing</sch>	Onery Match 8.5%: Score 96: DB 2: Length 149:

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protein B0238.12 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: H89044
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Fitle: Genome sequence of the nematode C. elegans: a platform for investigating biology A;Fitle: Genome sequence of the nematode C. elegans: a platform for investigating biology A;Fitle: websites genome.wust1.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/A;Note: spublished errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 24-May.1996 #sequence_revision 24-May-1996 #text_change 24-Sep-1999
C;Accession: A55499
G;Accession: A55499
A;Telte: Mouse cellular nucleic acid binding proteins: a highly conserved family identifi A;Reterence number: A55499; MUID:95203870; PMID:7896269
A;Reterence number: A55499; MUID:95203870; PMID:7896269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:016488; GB:chr_V; PIDN:AAB65990.1; PID:g2315490; GSPDB:GN0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 NSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 VSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDT--DCG-TCLPGFYEHGDGCVSCPTST 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----SĊTTPR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 GCYVYAQDAQILPVGGQVGGGQRLP-CRGRNEEYKTCGTACEPSCTNPNPM---CTKQCI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 GCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 NNVC-QCRSGYV---RNEITRQCVRQAQCS-------RPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A,Molecule type: mRNA
A,Residues: 1-170 <RES>
A,Cross-references: GB:L12693; NID:g292347; PIDN:AAA89198.1; PID:g292348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
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84 -TCCRPTCCRPTSCQTTCCRTQCCRPSC-----CVSTCCRPCCSSGSC 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----RNETFRTCGSSCEP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:125342; OMIM:116955
A;Map position: 3q13.3-3q24
C;Superfamily: cellular nucleic acid-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match
T.9%; Score 89.5; DE
Local Similarity 23.3%; Pred. No. 6.1;
les 45; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zinc finger protein 9 - human N; Alternate names: nucleic acid binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 -TGFGSSTPFPSQSPQRCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 LGSCPERCAA-VC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POACTMOCIVNVC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Residues: 1-166 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB: ZNF9
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Best Local S:
Matches 45,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cysteine-rich hair keratin associated protein - rabbit
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C.Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C.Accession: 146489; MA201
R.Powell, B.C.; Arthur, J.; Nesci, A.
Differentiation 58, 227-232, 1995
A.Title: Characterization of a gene encoding a cysteine-rich keratin associated protein
A.Reference number: 146489; MUID:95228955; PMID:7536172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q28707; EMBL:X80035; NID:g510540; PIDN:CAA56339.1; PID:g5109
C;Genetics:
                                                                                                                                                                                               C,Accession: S70007 "Ograni, C.; Wilcox, E.R.
R;Rivolta, M.N.; Negrini, C.; Wilcox, E.R.
Biochim. Biophys. Acta 1306, 127-132, 1996
A;Title: A novel zinc finger gene preferentially expressed in the retina and the organ A;Reference number: S70006; WUID:96221281; PMID:8634327
A;Accession: S70007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q15914; EMBL:L41669
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C;Keywords: zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 VCPQDTFLAWENH-----HNSE----CARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLC-----SRRDTDCGTCLPGFYEHG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 QACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA
A;Residues: 1-183 <RIV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 RDHTGEKVYKCDDCGKDFSTTTKLNRHKKI------HTVEKPYKCYB-CGKA--- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 CAGDFHKKIGLFCCR-GCPAGHYLKAPCTEP-CGNSTCLVCPQDTFLAWENHHNSECARC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- SSCCRP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 RAQGGTRSPRC-DCAGDF-----HKKIGLFCCRGCPAGHYLKAP--CTEPCGNSTCL 71
                                                                                                               finger protein zfOC1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.3%; Score 94; DB 2; Length 183; Best Local Similarity 21.7%; Pred. No. 3; Matches 43; Conservative 16; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 8.0%; Score 90; DB 2; Length 126; Local Similarity 25.4%; Pred. No. 4.7; es 43; Conservative 9; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 GGDFCQEES--CCRPSC----CRPQCCQPSCCRPTCI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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C,Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 SLCIHORVHT-GEKPYRC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 DGCVSCPTSTLGSCPERC 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73
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13;

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----GCGP----SCCVPVCC 146

-----GCSOSSCCRPCCSOSSC 181

---CGK--GGCGSC---

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72 VCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCV 131
                                                                                                                                                                                 63 GCSSCGGSKGSCGSCGG----CGSSCCKPVCCCVPVCSCSSCGKGGCGSSCGGSKGGCG 117
                                                                                                                                                                                                                                                                                                                                                             132 SSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGC--VSC--PTSTLGSC 187
                                                                                                                         21 GARAQGGTRSPRCDCAGDFHKKIGLFCCRG-----CPAGHYLKAPCTEPCGNST--CL
      th 7.9%; Score 89.5; DB 2; Length 191; Similarity 22.3%; Pred. No. 6.7; 42; Conservative 8; Mismatches 61; Indels 7
                                                                                                                                                                                                                                                                                                        118 SC-----GGSKGGCGSCGCCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: June 27, 2005, 14:02:57
                                                                                                                                                                                                                                                                                                                                                                                                                     147 -----CVPACSCSS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 PERCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 --- CVPVC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Job time : 44 secs
         Query Match
                                     Best Local
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                      cellular nucleic acid binding protein clone 6 - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 02-0ul-1996 #sequence revision 02-0ul-1996 #text_change 09-0ul-2004 C; Accession: 148297; S19861; S19959 R; Warden, C.H.; Krisans, S.K.; Purcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; T A; Tile: Mouse cellular nucleic acid binding proteins: a highly conserved family identif A; Reference number: A55499; MUD:95203870; PMID:7896269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Warden, C.H.
submitted to the EMBL Data Library, January 1992
A;Description: Cellular nucleic acid binding protein (CNBP) is an extremely conserved cy
A;Reference number: S19861
A;Accession: S19861
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C.Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C.Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C.Jaccession: 146412; A3215
J. Invest. Dermatol. 103, 310-317, 1994
J. Invest. Dermatol. 103, 310-317, 1994
A;Title: Differential expression of genes encoding a cysteine-rich keratin family in the A;Reference number: 146412; MUID:94358466; PMID:7521375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT:P53996; EMBL:Z11870; NID:g50472; PIDN:CAA77896.1; PID:g50473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 CKEPKREREQC----CYNCGKPGHLARDCDHADB-QKCYSCGEFGH--IQKDCTKVKCYR 132
                                                                                                                                80 CKEPEKEREQC----CYNCGKPGHLARDCDHADE-QKCYSCGEFGH--1QKDCTKVKCYR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTEP-----CGNSTCLVCPQDTFLAWENHINSECARCOACDEQASQVALENCSAVADTR 114
                                                                                          CTEP-----CGNSTCLVCPQDTFLAWENHHNSECARCOACDEQASQVALENCSAVADTR 114
29 MRSRGRGFQFVSSSLPDICYRC-GESGHIAKDCDLQED-----ACYNCGRGGHIAKD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 MRSRGRGFQFVSSSLPDICYRC-GESGHIAKDCDLQED-----ACYNCGRGGHIAKD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X63866; NID:g50470; PIDN:CAA45345.1; PID:g50471
C;Superfamily: cellular nucleic acid-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 170;
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                                                                                                                                                                                                                                                      | | : | | : | | CG-ETGHV----AINCSKTSEVNCYRCGESGHLAR 162
                                                                                                                                                                                                          115 CGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 CGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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Best Local Similarity 25.2%; Pred. No. 6.2;
Matches 39; Conservative 18; Mismatches
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C,Superfamily: ultra-high-sulfur keratin
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A; Residues: 1-170 < WA2>
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63 EPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQASQVALENCSAVADTRCGCKPGWF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---OYRYYWSETHFQCLNCSLC--LNGTVQISCKETQNTVCTCHAGFFLRGNECVSC 182
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Felis.
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08bdc6
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068wr4
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099x31
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; U72344; AAB5089.1; --
RASP; P19438; LEXT.
RGJ; GO:0004872; F:receptor activity; IEA.
RINEAPRO; IPR000345; CytC, heme_BS.
RINEAPRO; IPR000345; CytC, heme_BS.
RINEAPRO; IPR001369; TNFR_c6.
R Pfam; PF000209; TNFR, 3.
R SMART; SM00209; TNFR; 3.
R RASITE; PS00190; CYTOCHROWE C; UNKNOWN_1.
R PROSITE; PS01186; EGF 2; UNKNOWN_1.
R PROSITE; PS00509; TNFR_NGFR 1; 3.
R PROSITE; PS00509; TNFR_NGFR 1; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.5%; Score 198; DB 2; Length 18
29.4%; Pred. No. 5.3e-09;
ive 19; Mismatches 90; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Carnivora, Fissipedia, Pelidae,
NCBI_TaxID=9685,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2004 (TrEMBLrel. 06, Last sequence update) Tumour necrosis factor receptor p60 (Fragment).
                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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Q9PWX3
Q9PZS8
Q9BDC6
Q9BDC6
Q6SWR4
Q6SWX0
Q9PWY0
Q9PX94
Q9PZR0
Q9PZR1
Q9PZR7
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SEQUENCE
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1130
1 MEQRPRGCAAVAAALLLVLL......CVSCPTSTLGSCPERCAAVC
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Q8m120
Q9w1b4
Q9yp87
Q9yp87
Q9yp87
Q9jke0
Q8q51
Q8q51
Q8q51
Q8q51
Q8pxs2
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Q9pxs2
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0910w9
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Q9r230
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                         1612378 segs, 512079187 residues
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Q9R230
TR23 MOUSE
Q8MJZ0
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             protein search, using sw model
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Q6VZR1
Q9PZS2
Q8SQ49
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Q9BBC5
Q9PZS1
Q9PZS3
Q910W9
Q911R4
Q99IR4
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Gapop 10.0 , Gapext 0.5
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Q9PZS5
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1: uniprot_sprot:*
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length: 195
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164.5

Result No.

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80

Minimum I Maximum I

Database

Perfect score:

Sequence:

OM protein -

Run on:

Scoring table:

Searched:

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Gaps

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60 KVKDCTTSGGAPTCHPCTEGEEYTDRKHYSDKCRRCAFCDEGHGLEVETNCTRTQNTKCR 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 AALLLVLLG----ARAQG-----GTRSPRCDCAGDFHKKIGLFCCRGCPAGHY 56
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Q9ER63; Q87HC0;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1 tumor necrosis factor receptor superfamily member 23 precursor (Tumor necrosis factor receptor p60 homolog 1) (TNF receptor family member SOB) (Decoy TRAIL receptor 1) (TNF receptor homolog 1).

Name=Thfr8523; Synonyms=Dctrailr1, Thfrh1, Thfr811al1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=129/Sv; TISSUE=Embryonic stem cells; STRAIN=129/Sv; TISSUE=Embryonic stem cells; STRAIN=20519229; PubMed=11063728; DOI=10.1093/hmg/9.18.2691; Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R., Lane N., Raik W., Walter J.; "Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended imprinting.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=12466268; DOI=10.1074/jbc.M210783200; Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A., Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A., Gong D., Dobles M., Hetrig S., Hofmann K., Van Vlijmen H., Hsu Y.-M., Burkly L.C., Tschopp J., Zheng T.S., "Identification of a new murine tumor necrosis factor receptor locus that contains two novel murine receptors for tumor necrosis factor-related apoptosis-inducing ligand (TRAIL).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND 3D-STRUCTURE MODELING OF 52-160.
STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                          15.3%; Score 173; DB 2; Length 150; 28.9%; Pred. No. 5.5e-07; ive 16; Mismatches 66; Indels 3
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Pan G., Mao W., Risser P.;
"Characterization of SOB, a member of the TNFR family.";
     GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                       150 AA; 16644 MW; 7DEC76EC40A6BA4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 CKPGWFVECQVSQCVSSSPFYCQPCLDCG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 CKENFY--CNASLC-----DHCYHCTSCG 141
                                                                                                                                                                 Pfam; PF00020; TNFR C6; 2.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1.
PROSITE; PS50050; TNFR NGFR 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hum. Mol. Genet. 9:2691-2706(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43; Conservative
                                                                                                                                                                                                                                                                                                                                                                   150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                           Receptor.
NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
           셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 EPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKFG-- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ---WFVECQVSQCVSSSPFYCOPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 RFYW------SETLFQCNNCSLC--LNGTVQISCQEKQNTICTCHAGFFLREHECV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 VLLALLLEIYPISVTALVPHPRNRVKRAILCPQGKYIHPQDDSICCTKCHKGTYLYNDCP 73
                                                                                                                                                                                                                                                                         TISSUE=Brain;
MEDLINE=21109092; PubMed=11182158; DOI=10.1016/S0165-2427(00)00261-0;
Campbell S.E., Nasir L., Argyle D.J., Gault B.A., Duthie S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 VAAALLLVLLGARAQGGTRSPR-----CDCAGDFHKKIGLFCCRGCPAGHYLKAPCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Gaps
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-Wistar; TISSUE-Corpus luteum;
Lareu R.R., Dharmarajan A.;
Submitred (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AFI040914; AAD20221.1; -.
HSSP; Q92956; 1UMA.
GO; GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 189
189 AA; 21324 MW; 5D3AD6A5676BFE99 CRC64;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumor necrosis factor receptor p60 (Fragment)
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Pas receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                               "Cloning of canine IL-1ra, TNPR and TIMP-2.";
Vet. Immunol. Immunopathol. 78:207-214(2001).
EMBL, AR013955, AA001516.1; ...
HSSP, P19438; ITWR.
GO, GO:0004872; F:receptor activity; IEA.
InterPro; IPR000345; CytC heme BS.
InterPro; IPR001569; EGF Tike.
InterPro; IPR001569; TNPR G6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.4%; Score 197; DB 2; 28.6%; Pred. No. 6.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM0208; TNFR; 3.

PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.

PROSITE; PS01186; EGF 2; UNKNOWN 1.

PROSITE; PS00652; TNFR NGFR 1; 3.

PROSITE; PS50050; TNFR NGFR 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 SC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sc 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
SEQUENCE
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01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Orthopoxvirus.
NCBL_TaxID=10245;
                                         NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                         Receptor.
NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its modified ann-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 CCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALEN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 CCKTCPSGTFVKAPCKIPHTQGQCBKCHPGTFTGKDNGLH-DCBLCSTCDKDQNNVA--D 105
                                                                                                                                                                                                                                                                                                                                                                                                                                Removed in mature form (Potential).

GPI-anchor amidated cysteine (Potential).
TNPR-Cys 1.

TNFR-Cys 2.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Lacks a cytoplasmic death domain and hence is not capable of inducing apoptosis. May protect cells against TRAIL mediated apoptosis through ligand competition. Cannot induce the NF-kappa-B pathway.
-!- SUBCELLUIAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: Contains 3 TNPR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
Whinked (Glacky. . . ) (Potential).
                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00652; TWPR NGFR 1; 3.
PROSITE; PS50050; TWPR_NGFR_2; 2.
Glycoprotein; GPI-anchor; Lipoprotein; Receptor; Repeat; Signal.
                                                                                                                                                                                                                EMBL; AJ278264; CAC16405.1; -.
EMBL; AJ276505; CAC27352.1; -.
EMBL; AJ276505; CAC27352.1; -.
EMBL; AX165625; AAN87805.1; -.
EMBL; AX164550; AAL05072.1; -.
HSSP; Q92956; LJMA.
MGD; MG1:1930269; Thfref23.
GO; GO:0005031; F:tumor necrosis factor receptor activity; IDA.
InterPro; IPR001368; TNFR. G6.
Pfam; PF00020; TNFR. G6; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.6%; Score 164.5; DB 1; Length 176; ilarity 33.7%; Pred. No. 3.2e-06; Conservative 15; Mismatches 41; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                         Tumor necrosis factor receptor superfamily member 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 CSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 CSATSDRKCECQIGLY-----YYDPKFPESCRPCTKC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Fas receptor CD95 (Fragment).
Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                             SMART; SM00208; TNFR; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
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Best Local S
Matches 33
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DISULFID
DISULFID
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
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44 GLECCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVA 103
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"Vaccinia virus encodes a soluble and cell surface tumour necrosis
"vaccinia virus encodes a soluble and cell surface tumour necrosis
tfactor receptor that contributes to viral virulence.";

Virology 292:285-298(2002).

R MSBL, AJ416893; CAC95181.2; -.

R MSBL, AJ416893; CAC95181.2; -.

R GO; GO:00046020; C:membrane, IEA.

GO; GO:0006015; P:emportonia; IEA.

GO; GO:0006915; P:ammune reseponse; IEA.

GO; GO:0007165; P:signal transduction; IEA.

R GO; GO:0007165; P:signal transduction; IEA.

R PFAM: FP00020; TNRR C6; 2.

R PRINTS; RR01680; PASRECEPTOR.

R SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 GQFCRNPCPPGERKARDCTVNEDBPDCVPCQEGKEYTDKGHFSSKCRRCRLCDEGHGLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Vaccinia virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                            SEQUENCE FROM N.A.
Petit F., Arnoult D., Lelievre J.-D., Lecossier D., Hance A.J.,
Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=USSR;
MEDLINE=21874859; PubMed=11878931; DOI=10.1006/viro.2001.1236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 14.3%; Score 161.5; DB 2; Length Local Similarity 31.7%; Pred. No. 4.5e-06; les 32; Conservative 12; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                 Estaquier J.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF530075; AAM95635.1; -.
HSSP; 014763; 1DU3.
                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:tranamembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008063; Pas receptor.
InterPro; IPR008063; Pas receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 AA; 14814 MW; 91542C61323F3C27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 EINCTRIQNIKCRCKFNFF-----CNSAVCEHCDPCTKC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 LENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00020; TWFR_c6; 2.
PRINTS; PR01680; FASRECEPTOR.
SARAT; SM00208; TWFR; 2.
PROSITE; PS00652; TWFR NGFR 1; UNKNOWN_1.
PROSITE; PS50050; TWFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumour necrosis family receptor.
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186 AA
  153 LLCSRRDTDCGTCLPGFYEHGDG-CVSC 179
                                       136 --IPKRRCPCG-YFGGIDEQGNPICKSC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0004872; F:receptor activity; IEA.
Pfan, PF00020; TNFR C6.
SMART; SM00208; TNFR; 2.
SMART; S000522; TNFR NGFR 1; UNKNOWN_2.
PROSITE; PS00522; TNFR NGFR 2; 2.
SEQUENCE 186 AA; 20482 MW; D2342F1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186
                                                                                                                                                                                                      Created)
                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=GRI-90;
MEDLINE=97068532; PubMed=8963248;
                                                                                                                                                                                                    07,
                                                                                                                                                                                                                         07,
26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virology 243:432-460(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39; Conservative
                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel.
                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               Orthopoxvirus.
NCBI_TaxID=10243;
                                                                                                                                                                                                                                                                      A56R protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126
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Q9YP87
ID Q9YP8
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                                                                                                                                                                                                                                                                                                                         94 RKCPTGSFDKV--KCTGTQNSKCSCLPGWYCATDSSQ-----TEDCRDC----- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 QACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTR 152
                                                                                                                                                                                                                                                                                             93 QACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTR 152
                                                                                                                                                                                                                                33 CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARC 92
                                                                                                                                                                                                    33 CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 CD-EGEYLDKRHNOCCNOCPPGEFAKVRCNGN-DNTKCERCPPHTYTAIPNYSNG-CHOC
                                                                                                                                                          25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccinia virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=9922647; PubMed=10211965;
Macani A., Khanna A., Pauli N., Smith J.L.;
Alcani A., Khanna A., Pauli N., Smith J.L.;
"Vaccinia virus strains Lister, USSR and Evans express soluble and
cell-surface tumour necrosis factor receptors.";
J. Gen. Virol. 80:949-959(1999).
EMBL; Y17728; CAB41042.1; -.
                                                                                                           Query Match 13.9%; Score 157.5; DB 2; Length 186; Best Local Similarity 28.4%; Pred. No. 1.3e-05; Matches 42; Conservative 17; Mismatches 64; Indels 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.9%; Score 157.5; DB 2; Length 186; 28.4%; Pred. No. 1.3e-05; ative 17; Mismatches 64; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptoais; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; TNTR_G6.
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                                                                 20662 MW; EF73D6A336A70C5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumour necrosis factor receptor precursor.
                                                                                                                                                        64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 AA.
                                                                                                                                                                                                                                                                                                                                                                                    153 LLCSRRDTDCGTCLPGFYEHGDG-CVSC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                --IPKRRCPCG-YFGGIDEQGNPICKSC 160
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PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 2.
PR0SITE; PS00652; TNFR, NGFR 1; 2.
PROSITE; PS50050; TNFR NGFR_2; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
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nes 42; Conservative
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                                                                   186 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=A53R;
                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 CD-EGEYLDKRHNOCCNOCPPGEFAKVRCS-GSDNTKCERCPPHTYTAIPNYSNG-CHQC 93
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                                                                                                                                            Cowpox virus (CPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=GRI-90; MEDLINE=98229462; PubMed=9568042; DOI=10.1006/viro.1998.9039; Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A., Ryazankina O.I., Gutorov V.V., Kotwal G.J.; Species-specific differences in genome organization of cowpox, smallpox, and vaccinia viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=GRI-90;
Shichelkunov S.N., Safronov P.F., Totmenin A.V., Miheev M.V.,
Shachelkunov S.N., Safronov P.F., Totmenin A.V., Miheev M.V.,
Sazankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J.,
Sandakhchiev L.S.;
Submitted (MaR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, X94355; CAD90723.1;
HSSP, Q92956; LJMA.
                                                                                                                                                                                                                                                                                                                                                                                                                     Safronov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V., Shchelkunov S.N., Sandakhchiev L.S., "Genes of a circle of hosts for the cowpox virus."; Dokl. Akad. Nauk 349:829-833(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- SSQTEDCRDCVPK-----SRCPCGYFGGIDEQGNPIC 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D2342F1040A00AE3 CRC64;
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%; Score 155; DB 2; 23.9%; Pred. No. 2.1e-05; cive 20; Mismatches 62;
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48 CRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQA-CDEQASQVALEN 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 RKCPTGSFDKV--KCTGTQNSKCSCLPGWF-----CATDSS-KTEDCRDC----- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 CNQCPPGSYVKQHCT-AASPTVCAPCP-DQYYAEDWNSNDECQYCSAVCKE--LQYIKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-22760275; PubMed-12878204; DOI=10.1016/S0006-291X(03)01304-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endopment J.T., Johnson A.L.;

Endopmental J.T., Johnson A.L.;

Endopmental J.T., Johnson A.L.;

And Osteoprotegerin.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 AA; 16487 MW; 1C9E64FE3A0FC2DF CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUNA-2004 (TrEMBLrel. 26, Last annotation update)
CD40 protein (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and osteoprotegerin.";
Biochem. Blobhys. Res. Commun. 307:956-961(2003)
EMBL. AX251407; AAP03890.1; --
HSSP; O14763; 1D4V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR06209; EGF like.
InterPro; IPR001368; TWFR_G6.
Pfam; PF00020; TWFR c6; 2.
SWART; SW00208; TWFR; 3.
PROSITE; PS01186; EGF2; UNKNOWN_1.
PROSITE; PS00622; TWFR NGFR_1; 1.
PROSITE; PS50050; TWFR_NGFR_1; 1.
                                                                   153 LLCSRRDTDCGTCLPGFYEHGDG-CVSC 179
                                                                                                                       136 --IPKRKCPCG-YFGGIDELGNPLCKSC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-Wistar; TISSUE=Smooth muscle;
                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                       Osteoprotegerin (Fragment).
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                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                   Q7ZZY4;
01-JUN-2003 (
01-JUN-2003 (
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                                                                                                                                                                                                             RESULT 10
Q7ZZY4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Brighton Red;
MEDLINE=94378510; PubMed=8091665;
Hu F.Q., Smith C.A., Pickup D.J.;
"Cowpox virus contains two copies of an early gene encoding a soluble
secreted form of the type II TNF receptor.";
Virology 204:343-356(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAMENHHNSECARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Brighton Red;
MEDLINE=9196263; PubMed=2014645;
Hu F.O., Pickup D.J.;
"Transcription of the terminal loop region of vaccinia virus DNA is initiated from the telomere sequences directing DNA resolution.";
Virology 181:716-720(1991).
                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Brighton Red;
MEDLINE=83117629; PubMed=6961398;
MEDLINE=83107629; PubMed=6961398;
MEDLINE=83107629; PubMed=6961398;
"Sequence of terminal regions of cowpox virus DNA: arrangement of repeated and unique sequence elements.";
Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parsons B.L., Pickup D.J., "Transcription of orthopoxvirus telomeres at late times during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 186;
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Brighton Redgene;
Smith C.A. Goodwin R.G., Pickup D.J.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Soluble TNF receptor CrmC (CrmC or CPXV191 protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; Q92956; LDWA.
GO; GO:0004872; F:receptor activity; IEA.
Threarpo; IPR001368; TNFR.c6.
Pfam; PF00020; TNFR.c6; 2.
SMART; SM00208; TNFR; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Brighton Red;
MEDLINE=90177240; PubMed=2309453;
                                                                                                                          Name=crmC; Synonyms=CrmC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virology 175:69-80(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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STRAIN=Brighton Red;
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nes 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                   Cowpox virus (CPV)
                                                                                                                                                                                                                                         NCBI_TaxID=10243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE
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83 NHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 NHHNSECARCQACDEQASQVALENCSAVADŢRCGCKFGWFVECQVSQCVSSSPFYCQPCL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 SHFSPRCRRCKICDEEHGLEVEKNCTRTQNTKCRCKSNFF--CNVSQC----DHCNPCM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 SHFSPRCRRCKICDEEHGLEVEKNCTRTQNTKCRCKSNFF--CNVSQC-----DHCNPCM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
"Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
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                                                                                                                                                                                                                                                                                                                                                                                                 11.8%; Score 133.5; DB 2; Length 124; 29.4%; Pred. No. 0.00096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.8%; Score 133.5; DB 2; Length 29.4%; Pred. No. 0.0011; tive 12; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 DCGALHRHTRLLCSRRDTDCGTCLPGFYEHG--DGCVSCPTS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 DCGALHRHTRLLCSRRDTDCGTCLPGFYEHG--DGCVSCPTS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; TNFR_C6.
          GO:0004888; F:transmembrane receptor activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------EHGILENCT--PTS 76
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                                                                                                                                                                                                                                                                                                                                                 124 AA; 14319 MW; 15A7DFF058D79942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
GO; GO:0004888; F:transmembrane reception GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:00007165; P:asgnal transduction; IEA.
InterPro; IPR001363; Fas_receptor.
InterPro; IPR001363; Fas_receptor.
R PEm; PF000120; TNFR c6; Z.
RRINTS; PR01680; FASRECEPTOR.
R PRINTS; PR01680; FASRECEPTOR.
R PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1.
R PROSITE; PS00652; TNFR NGFR 2: Z.
TNFR NGSTER; PS00652; TNFR NGFR 2: Z.
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PROSITE; PS00652; TNFR NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
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Felis silvestris catus (Cat).
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PRINTS; PR01680; FASRECEPTOR.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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Eur. J. I
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 CGNSTCLVCPQDTFLAWENHHNSE--CARCQACD-EQASQVALENCSAVADTRCGCKPGW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 PRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 POLCALWGCLLTAVHLG------QCVTCSDKQYLQGGECCDLCQPGNRLVSHCT-A 53
        MEDLINE=99330195; PubMed=10403401; DOI=10.1016/S0014-5793(99)00683-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31, Gaps
                             Krzesz R., Wagner A.H., Cattaruzza M., Hecker M.;
"Cytokine-inducible CD40 gene expression in vascular smooth muscle
cells is mediated by nuclear factor kappaB and signal transducer and
activator of transcription-1.";
FEBS Lett. 453:191-196(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 FVECQVSQCVSSSPFYCQPCLD---CGALHRHTRLLCSRRDTDCGTCLPGFYEHG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----QHCASKE---CETCAQHRPCGPGFGVVQMATETTDTVCQPCPVGFFSNG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
"Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Fas delta6 (Fragment).
Felis silvestris catus (Cat).
Felis silvestris catus (Cat).
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.2%; Score 137.5; DB 2; Length 169; 29.1%; Pred. No. 0.00058; tive 15; Mismatches 78; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO, GO: 0016020; C: membrane; IEA.
GO; GO: 0016020; C: membrane; IEA.
GO; GO: 0006915; P: papprobals; IEA.
GO; GO: 0006915; P: papprobals; IEA.
GO; GO: 0006915; P: papprobals; IEA.
GO; GO: 0007165; P: signal transduction; IEA.
InterPro; IPR008065; Fa Ecceptor.
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR001186; Ribosomal_S2.
InterPro; IPR001186; Ribosomal_S2.
FRINTS; PR016000; TNFR. G6; 1.
FRINTS; PR01600; FASRECEPTOR.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Wister; TISSUB-Smooth muscle;
Krzesz R., Hecker M. Hecker
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                           STRAIN=Wistar; TISSUE-Smooth muscle;
Gao D., Hecker M.;
Submitted (WAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF241211, AAF43717.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON TER 169 169" - SEQUENCE 169 AA; 18525 MW; F199D91EFA224A26 CRC64;
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PROSITE; PS00652; TWPR NGFR_1; 1.
PROSITE; PS50050; TWFR_NGFR_2; 3.
NON_TER
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Eur. J. Immunogenet. 31:159-166(2004).
EMBL; AB072010; BAB86799.1; -.
HSSP; O14763; 1D0G.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                      Canarypox virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC VR-111;
PubMed=14671117; DOI=10.1128/JVI.78.1.353-366.2004;
Fulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
The genome of canarypox virus.";
J. Virol. 78:353-366 (2004).
EMBL; AY318871; AAR83432.1; -.
EMBL; AY318871; AAR83432.1; -.
InterPro; IPR06209; EGF like.
InterPro; IPR001368; TNFR G6.
InterPro; IPR001209; TNFR G6. 1.
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Lurain N.S., Kapell K.S., Huang D.D., Short J.A., Paintsil J.,
Winkfield E., Benedict C.A., Ware C.F., Bremer J.W.;
"Human cytomegalovirus UL144 open reading frame: sequence
hypervariability in low-passage clinical isolates.";
J. Virol. 73:10040-10050(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.7%; Score 132; DB 2; Length 117; llarity 26.0%; Pred. No. 0.0012; Conservative 24; Mismatches 53; Indels
--EHGILENCT--PTS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00208; TNFR; 2.
PROSITE; PS01186; EGF 2; UNKNOWN 1.
PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1.
PROSITE; PS500505; TNFR NGFR 2; 1.
SEQUENCE 117 AA; 13113 MW; 06E99CAB6A41135A CRC64;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
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Name=CNPV086;
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nes 32; Conser
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NCBI TaxID=44088;
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                         63 MC-
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DT 01-MAP
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COC Betah
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DR HSSP; 029256; 1J7A.

DR HSSP; 029256; 1J7A.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPRO01368; TRFR_c6.

DR SMART; SM00208; TRFR_c6.

DR SMART; SM00208; TRFR_c6.

DR PROSITE; PS:0050; TRFR_NGFR_1; UNKNOWN_1.

DR PROSITE; PS:0050; TRFR_NGFR_1; UNKNOWN_1.

DR PROSITE; PS:0050; TRFR_NGFR_2; 1.

Query Match

Best Local Similarity 33.3%; Pred. No. 0.0037;

Matches 31; Conservative 15; Mismatches 35; Indels 12; Gaps 6;

Aggresprocrapperticecrecopactive conservative 15; Mismatches 35; Indels 12; Gaps 6;

Oy 26 GGTRSPRODEAGHYLKGLFCCRECOPACHYLKAPCTEPCGNSTCLVCPODTFLAWENHH 85

DS 18 GSSKM---CKPD-EVKLGNGCCPPGSGGKYTKVCTENSG-ITCTLCPNGTYLT--GLY 69

CY 86 NSECARCQACDEQASQVALENCSAVADTRCGCK 118

DD 70 N--CTNCTQCDD--TQITVRNCTSTNNTICASK 98

Search completed: June 27, 2005, 13:59:20

Job time: 172 secs
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Truncated Rat Fas r Human TRA Human TR2

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This novel polypeptidede, designated Apo-2 ligand inhibitor (Apo-2LI), can be used to inhibit apoptosis for therapeutic purposes. Its amino acid sequence was deduced from a human thymus CDNA clone (see AAT91179) and is identical to amino acid residues 1-181 of another novel apoptosis polypeptide, Apo-3 (see AAW26709). It may be a soluble, truncated of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis in
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N-PSDB; AAT91179.
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                            the transmembrane and cytoplasmic sequences of Apo-3. Apo-2LI can be produced in host cells using a claimed method. Chimeric polypeptides comprising Apo-2LI fused to a heterologous amino acid sequence, and an Apo-2LI dimer are also claimed. Apo-2LI can be used to inhibit mammalian cell apoptosis in vivo or ex vivo, and in quantitative diagnostic assays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APO-2LI; human; apoptosis; monoclonal antibody; Apo-2 ligand inhibitor; cytostatic; cancer; autoimmune; inflammatory; neurodegenerative disease.
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   extracellular sequence as
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secreted form of Apo-3, lacking
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96US-00710802.
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N-PSDB; ABX15839.
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                                                                                                                                                                                                                                          Sequence 181 AA;
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C-Jun-amino-terminal kinase (JNK) activation. The anti-Apo-2 ligand inhibitor is useful in therapeutic purposes for activating or stimulating apoptosis in cancer cells and may be used to block excessive apoptosis (for example in neurodegenerative disease), or to block potential autoimmune/inflammatory effects of Apo-3 resulting from nuclear factor (NF)-kappaB activation or C-Jun-amino-terminal kinase (JNK) activation. The antibody may also be used in diagnostic assays for Apo-2LI or Apo-3, e.g. detecting Apo-2LI or Apo-3 expression in specific cells, tissues or serum, or for affinity purification of Apo-2LI or Apo-3 from recombinant cell culture or natural sources. The present sequence represents the human Apo-2 ligand inhibitor protein (Apo-2LI) which was used to generate the antibody of the invention
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                                                                                                                                                                                                                                                                            Length 181;
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                                                                                                                                                                                                                                                                          93.0%; Score 1051; DB 6;
100.0%; Pred. No. 4.8e-72;
iive 0; Mismatches 0;
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97US-00829270.
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Matches 181; Conservative
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N-PSDB; ABX13176.
                                                                                                                                                                                                                                           Sequence 181 AA;
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                                                    The invention relates to an new isolated biologically active Apo-2LI or Apo-3 having at least 80 % sequence identity with native sequence Apo-2LI or Apo-3 appearing as ABU08251 and ABU08252. Also included are a confinaeric molecule comprising the Apo-2LI fused to a heterologous amino acid sequence; a dimer molecule comprising a first Apo-2LI and a second Apo-2LI, an antibody that binds to Apo-2LI or Apo-3 for to its certacellular domain sequence), an isolated nucleic acid encoding Apo-2LI or Apo-3, a vector comprising the nucleic acid, a host cell comprising the nucleic acid, a host cell comprising the nucleic acid, a host cell comprising the vector, a method of producing Apo-2LI and a non-human (transgenic or Apo-3, a vector and attendance cell death) which is implicated in cells having an altered gene encoding Apo-3 or cells having an altered gene encoding Apo-2LI cand a non-human (transgenic or Apo-3 or cells having an altered gene encoding Apo-2LI or Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3 or cells having an altered sene encoding Apo-3 or cells having an altered sene encoding Apo-3. Apo-2LI or Apo-3 or cells having an altered sene encoding Apo-3 or cells having an altered sene encoding Apo-3. Apo-2LI or Apo-3 or cells having an altered sene encoding Apo-3 or cells having an altered sene encoding Apo-3. Apo-2LI or Apo-3 are also useful for preparing a composition for treating cancer. The present sequence represents Apo-2LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105
/note= "N-glycosylated. The amino acid at residue 105 is Glu not Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEQRPRGCAAVAAALLLVILGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toxin-induced liver disease; cancer; lupus; herpes virus infection
                                                                                                                                                                                                                                                                                                                                                                                                             93.0%; Score 1051; DB 6; Length 181; 100.0%; Pred. No. 4.8e-72; ive 0; Mismatches 0; Indels (
 preparing a composition for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Apo-2 ligand inhibitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG73857 standard; protein; 181 AA.
                             Claim 4; Fig 1; 45pp; English.
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Best Local Similarity 100.0
Matches 181, Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 181 AA;
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The invention relates to an Apo-3 polypeptide having an extracellular domain (BCD) sequence and a death domain sequence. The Apo-3 polypeptide domain (BCD) sequence and a death domain sequence. The Apo-3 polypeptide has been found to stimulate or induce apoptotic activity in mammalian cells. Human Apo-3 exhibits similarities to the tumour necrosis factor creceptor (TNFR) family of polypeptides. The invention also relates to a chimeric molecule comprising an extracellular domain sequence comprising residues 1-198 of Apo-3 luseful therapeutically to induce apoptosis in Apo-3 polypeptide is useful therapeutically to induce apoptosis in mammalian cells. Decreased levels of apoptosis are associated with diseases such as acquired conditions such as cancer, lugus, and herpes virus infection. Increased levels of apoptosis are associated with diseases such as acquired immunodeficiency syndrome (AIDS), Alzheimer's disease, anyotrophic lateral seclerosis, multiple sclerosis, retinitis pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial confinancion, stroke, reperfusion injury, and toxin-induced liver disease.

The Apo-3 polypeptide is also useful in non-therapeutic applications such as in quantitative diagnostic assays as a control against which samples containing unknown quantities of Apo-3 may be prepared, in generating antibodies, as standards in assays for Apo-3 in affinity purification containing unknown quantities of Apo-3 may be prepared, and in competitive-type receptor binding apoptosis or nuclear factor -kappa B (NF-kappa B) induction, or as an immunogen for producing anti-containing unknown quantities of apo-3 and immunogen for producing anti-containing unknown present sequence represents the human Apo-2 ligand inhibitor protein which comprises amino acid residues in to 181 of the human Apo-3 protein. It is believed that Apo-3 social in this believed that Apo-3 social in the form of Apo-3 social in this believed that Apo-3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated Apo-3 polypeptide useful for inducing apoptosis in mammalian cells, for generating antibodies, in affinity purification techniques, and in competitive-type receptor binding assays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3xample 1; Fig 1; 52pp; English
                                                                                                                                                                   97US-00928069.
                                                                                                                                                                                                                                                     96US-0026943P.
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                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-173840/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Ashkenazi AJ;
                                                                                                                                                                                                                                                         23-SEP-1996;
                                                                                                                                                                   11-SEP-1997;
US6462176-B1
                                                                                 08-OCT-2002.
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ADA49687 standard; protein; 181 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides are useful for stimulating or inducing apoptotic activity in mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy rechniques. The Apo-3 chimeric molecules are useful for inhibiting apoptosis, or as immunogens used in generating antibodies. The antagonistic antibodies may be used to block excessive apoptosis, for instance in neurodegenerative disease, or to block potential autoimmune/inflammatory effects of Apo-3 resulting from NP-kappaB activation. The nucleic acid sequences are useful as diagnostics for tissue-specific typing, for preparing Apo-3 polypeptides, or for generating transgenic or knockout animals. The transgenic or knockout animals are useful in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                  New isolated Apo-3 polypeptides, useful for stimulating or inducing apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo or ex vivo gene therapy techniques.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developing and screening of therapeutically useful reagents. The present sequence represents the amino acid sequence of human Apo-2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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                                                                                              Human; Apo-2 ligand inhibitor; apoptosis; gene therapy; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                          cancer; neurodegenerative disease; immunosuppresive; tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated Apo-3 polypeptide. The Apo-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.0%; Score 1051; DB 6; Length 181; 100.0%; Pred. No. 4.8e-72; ative 0; Mismatches 0; Indels (
ABU10202 standard; protein; 181 AA
                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 1; 50pp; English.
                                                                                                                                                                                                                              96US-0026943P.
97US-00928069.
                                                                       Human Apo-2 ligand inhibitor
                                                                                                                                                                                                       28-MAR-2002; 2002US-00112193
                                               11-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 181; Conservative
                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                 2003-438872/41.
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N-PSDB; ACA61684.
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                                                                                                                                                         JS2003004313-A1
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                                                                                                                                                                                                                               23-SEP-1996;
11-SEP-1997;
                                                                                                                                  Homo sapiens
                                                                                                                                                                                 02-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or Apo-3 polypeptide which induces or stimulates apoptotic activity, useful
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                                                                                                                   Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; affinity; competitive-type receptor; binding assay; cancer cell; human; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.0%; Score 1051; DB 6;
100.0%; Pred. No. 4.8e-72;
tive 0; Mismatches 0;
                                                         Human Apo-2 ligand inhibitor (Apo-2LI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-00625328.
96US-00710802.
97US-00828683.
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                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-2002; 2002US-00112793
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
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N-PSDB; ADA49691.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1996;
23-SEP-1996;
31-MAR-1997;
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                                                                                                                                                                                                                   Homo sapiens
20-NOV-2003
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Numour necrosis factor; receptor; TNFrED; proline; protein engineering;

mutant; mutein. sapiens

Synthetic.

/note= "wild-type Ser substituted by Ile" /note= "wild-type His substituted by Pro"

Misc-difference 46

WO2003046160-A2

05-JUN-2003

Misc-difference

Location/Qualifiers

Tumour necrosis factor receptor extracellular domain H23P

(first entry)

22-SEP-2003

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with rheumatoid arthritis. Certain mutations in the gene can be linked to the disease. The sequences can be used to evaluate disease onset and its possibility and to provide therapy and remedies. The present sequence is a protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the human DR3 gene, which is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomes, particularly DR3 genomic DNA, participating in rheumatoid arthritis via mutation, useful in evaluating disease onset and its possibility and providing therapy and remedies.
                                                                                                          Human rheumatoid arthritis associated DR3 gene related protein #2.
                                                                                                                                       Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 72-73; 84pp; Japanese
                        AA017880 standard; protein; 188 AA
                                                                                                                                                                                                                                                                 24-OCT-2001; 2001WO-JP009313.
                                                                                                                                                                                                                                                                                         24-OCT-2000; 2000JP-00324296.
27-MAR-2001; 2001JP-00090546.
30-MAR-2001; 2001JP-00099990.
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                    (NEWI-) NEW IND RES ORG
                                                                                                                                                                                                                                                                                                                                                                                             Konishi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-417132/44.
N-PSDB; AAL47187.
                                                                                                                                                                                                                                                                                                                                                                 (SHIO/) SHIOZAWA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 188 AA;
                                                                                                                                                                                                          WO200234912-A1
                                                                                22-AUG-2002
                                                                                                                                                                                                                                                                                                         27-MAR-2001;
30-MAR-2001;
                                                                                                                                                    gene therapy
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           Shiozawa S,
                                                                                                                                                                                                                                     02-MAY-2002
                                                    AA017880;
          RESULT 7
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Increasing expression of a protein, comprises substituting at least one codon in the polynucleotide encoding the protein, for a codon encoding

Example 2; Page; 53pp; English

proline

(ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

21-NOV-2002; 2002WO-EP013059 30-NOV-2001; 2001US-0340648P Schweickhardt RL;

Brondyk W, Jiang X, WPI; 2003-523245/49.

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120
                                                                                                                                                                                                 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                                                                                                                WEVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                              9
                                                                                        9
                                                                            1 MEORPRGCAAVAAALLIVLIGARAOGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
                                                            MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKK1GLFCCRGCPAGHYLKAP
                                                                                                                      CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG
                                Gaps
                                ö
93.0%; Score 1051; DB 5; Length 188; 100.0%; Pred. No. 5e-72; ive 0; Mismatches 0; Indels
 Query Match
Best Local Similarity 100.
Matches 181; Conservative
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ABR62365 standard; protein; 161 AA.

RESULT 8
ABR62365
ID ABR6
XX
AC ABR6

ABR62365

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This is the protein sequence of a mutated extracellular domain of the p55 tumour necrosis factor receptor (TNFTED) in which a Pro residue substitutes the native His-34 residue (residue 23 in the present sequence) and an Ile residue substitutes the native Ser-57 residue (residue 46 of the present sequence). Screening of TNFTED mutant clones using a yeast display system yielded a clone that showed a higher expression level in yeast than did a wild-type TNFTED clone. The encoded polypeptide contained these 2 amino acid substitutions. The introduction of proline residues may assist the polypeptide to adopt a favourable conformation that fixes the neighbouring cysteine residue into the correct orientation for disulfide bond formation, resulting in a higher invention therefore provides methods of increasing protein expression levels by substituting an amino acid residue with proline, where the substitution occurs within 15 (preferably within 10, and especially within 5) amino acids of a cysteine residue. Note: The present sequence is not shown in the specification but is derived from the TNFTED sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC-----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRDIDCGICLPGFYEHGDGCVSCPISILGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.3%; Score 206.5; DB 6; 30.4%; Pred. No. 4.4e-08; tive 20; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 161 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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human tumour necrosis factor(TNF)-receptor related protein TR2. Included human tumour necrosis factor(TNF)-receptor related protein TR2. Included human tumour necrosis factor(TNF)-receptor related protein TR2. Included to the the two splice variants of TR2. TR2-SV1.

The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a member of the TNFR superfamily. The invention includes a method for the treatment of arthritis or inflammation using an antibody directed against a fragment of the TR2 protein. TR2 its agonists and antibodies exhibit cytostatic, dermatological, antianaemic, antibodies exhibit cytostatic, dermatological, antianaemic, antibodies exhibit cytostatic, dermatological, antianaemic, antibodies exhibit cytostatic, antiantersthinstic, antibodies activity. The methods are useful for treating arthritis or inflammation, cancer (such as follicular lymphomas, carcinoma with p53 mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an immunodeficiency or for enhancing an in vivo leukocyte response to an immunodeficiency or for enhancing an in vivo leukocyte response to an antigen. Anti-TR2 antibodies are useful for treating, inhibiting or preventing autoimmune diseases (such as autoimmune haemolytic anaemia, dermaticis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and inflammatory myopathies) and immunodeficiency disorders (such as severely combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative combined immunodeficiency or preventing autoimmune diseases and inhibit the growth, progression and/or metastasis of cancers. They are altso used to activate, differentiate or proliferate cancerous cells or timibit the growth, progression and/or metastasis of cancers. They are also used to activate, differentiate or proliferate cancerous cells or tissues, and can be used to treat diseases associated with increased cell survival, or the inhibition of apoptosis, e.g. Alzheimers essentell
                                                                                                                                                                                                                  chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease; immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID; severely combined immunodeficiency; apoptosis inhibition; Alzheimer's disease; Parkinson's disease; Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid molecule encoding a human tumor necrosis factor receptor 2 and its two splice variants, useful for treating arthritis or inflammation, cancer (such as follicular lymphomas) and immunodeficiency
                                                                                                                                                                                               necrosis factor-receptor related protein; TR2; human; cancer;
                                                                                                                                                      Tumour necrosis factor receptor (TNFR) domain of TNFR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 16, 373pp, English.
                  AAY94711 standard; protein; 154 AA.
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99US-0126522P.
99US-0135169P.
99US-0147383P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAR-2000; 2000WO-US007521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gentz RL;
                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NI J.
ROSEN C A.
GENTZ R L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                            WO200056405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-1999;
                                                                                                          29-JAN-2001
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                                                                AAY94711;
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AAY9471
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                                                                                                                                                                                                                                                                                             100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                                                                                 68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or
Apo-3 polypeptide which induces or stimulates apoptotic activity, useful
in diagnostic assays.
as sources for generating antibodies, as molecular weight markers. This sequence represents the tumour necrosis factor receptor (TNFR) domain of the human TNFR-1 protein. The sequence was used in the characterisation
                                                                                                                                                                                                                   66
                                                                                                                                                                                                                                                       9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                   40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                              Gaps
                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apo-2 ligand inhibitor, Apo-2LI, Apo-3, apoptosis, affinity, competitive-type receptor; binding assay; cancer cell; human; TNF receptor family; hTNFR1; cytostatic.
                                                                                                                                        17.7%; Score 200.5; DB 3; Length 154; 29.8%; Pred. No. 1.2e-07; ive 20; Mismatches 72; Indels 21
                                                                                                                                                                                                                                                                                                                                                                          157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                Extracellular region of human TNFR1 (hTNFR1) protein.
                                                              of the TR2 receptor protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA49698 standard; protein; 154 AA
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96US-00710802.
97US-00828683.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                            48; Conservative
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                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS2002192729-A1.
                                                                                                    Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ashkenazi AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1996;
23-SEP-1996;
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ADA49698
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fragment of the amino acid residues 68-240 of the Human apoptosis
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21-MAR-1997;
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20-FEB-1998,
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02-DEC-1999;
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Best Local S
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                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                156
                                                                                                                                                                                                                                                                                                                                                                                 68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibody that binds to human Apoptosis Inducing Molecule II (AIM II) protein, useful for preparing a composition for treating e.g., lymphadenopathy, autoimmune disease, rheumatoid arthritis, osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated antibody or its portion binding to a protein comprising a protein whose sequence comprises an immunogenic
                                                                                                                                                                                                                                 66
                                                                                                                                                                                                                                                                                    9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                             100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS
                                                                                                                                                                                                                              40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQA
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour necrosis ligand superfamily, lymphotoxin-beta receptor, TR6, TRAIL receptor 6; lymphadenopathy, aberrant bone development; autoimmune disease; graft-versus-host disease; rheumatoid arthritis;
                                                                                                                                                                        Indels 21;
                                                                                                                     Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human tumour necrosis factor receptor-I cysteine rich motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; apoptosis inducing molecule II; AIM II; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72;
                                                                                                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhai Y;
                                                                                                            ; Score 200.5; DB (; Pred. No. 1.2e-07, 20; Mismatches 72)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 13; SEQ ID NO 53; 163pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL17741 standard; protein; 154 AA
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96US-0030157P.
97US-00023886.
98US-0007287.
98US-0075409P.
99US-00252656.
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99US-0137457P.
99US-0142657P.
                                                                                                            17.7%;
29.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAR-2000; 2000US-00523323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-2004 (first entry)
                                                                                                                                       Local Similarity 29.89 tes 48; Conservative
region of human Apo-2LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-810570/76.
                                                         Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6635743-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-AUG-1999;
02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-0CT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL17741;
                                                                                                               Query Match
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                                                                                                                                             Best Loc
Matches
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inducing molecule II, AIM II, appearing as ADL17690 or a protein whose sequence comprises a fragment of amino acid residues 68-240, where the fragment comprises at least 30 or 30 amino acid residues. Also included are a hybridoma that produces the antibody, a method of detecting in a biological sample a protein that binds the antibody or its portion, a composition comprising the antibody and a carrier and an isolated cell that produces the antibody. Human AIM II is a member of the tumour necrosis ligand superfamily and has been shown to bind lymphotoxin-beta receptor and TR6 (TRAIL receptor 6). The antibody is useful for preparing a composition for treating e.g., lymphadenopathy, aberrant bone development, autoimmune disease, graft-versus-host disease, rheumatoid arthritis, osteoarthritis or cancer (many other diseases and conditions are listed in the specification). The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 GQVEISSCTVDRDITVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myelodysplasia; systemic lupus erythematosus;
idiopathic thrombocytopenic purpura; cellular response;
T-cell activation; molecular weight marker; human; TNF receptor; TNFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.7%; Score 200.5; DB 7
29.8%; Pred. No. 1.2e-07;
iive 20; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ56814 standard; protein; 154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human TNFR-I cysteine-rich motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0030157P.
97US-00822953.
98US-0003886.
98US-00027287.
99US-00252656.
99US-0124041P.
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99US-0142657P.
99US-0148326P.
99US-0168380P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 29.8 48; Conservative
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(SYND ) SYNERGEN INC
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09-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                   The invention relates to apoptosis inducing molecule II (AIM II), a TNF (tumour necrosis factor)-ligand superfamily member and its corresponding nucleic acid sequence. The invention is useful for preventing, treating, ameliocating, diagnosing or prognosing graft versus host disease, immunodefictency, cancer, autoimmune diseases such as multiple sclerosis, type I diabetes, rheumatoid arthritis, primary biliary cirrhosis, aplastic anaemia, myelodysplasia, systemic lupus erythematosus and idiopathic thrombocytopenic purpura. It is useful for screening or identifying compounds capable of enhancing or inhibiting cellular response induced by AIM II, for inhibiting, blocking or reducing T-cell activation. AIM II is useful as a molecular weight marker on SDS-PAGE gels or on gel filtration columns. The present sequence is a cysteinerich motif of human TNF receptor (TNFR) family member.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                              Isolated apoptosis inducing molecule II polypeptide, useful for treating, preventing, ameliorating, diagnosing or prognosing autoimmune diseases such as multiple sclerosis, rheumatoid arthritis, aplastic anemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                            40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                                                                                                     21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INF; human; tumour necrosis factor; tumour necrosis factor receptor; INF-R; tumour necrosis factor binding protein; TNF-BP; tumour.
                                                                                                                                                                                                                                                                                                                                                                                           17.7%; Score 200.5; DB 8; Length 154; 29.8%; Pred. No. 1.2e-07; ative 20; Mismatches 72; Indels 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
                                                             Ullrich S;
                                                                                                                                                                 Example 13; SEQ ID NO 53; 189pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
                                                               Yu G, Ruben SM, Zhai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG74752 standard; protein; 161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human TNF binding protein fragment
10-MAR-2000; 2000US-00523323.
01-MAR-2002; 2002US-0360234P.
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                                    (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                    48; Conservative
                                                                                      WPI; 2004-201265/19.
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36-APR-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNF; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP393438-A.
                                                               Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                 This invention describes novel polynucleotide sequences encoding tumour necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP). The products of the invention are useful in pharmaceutical compositions for prophylaxis or treatment of human tumnours and to understand the mechanisms of TNF action. This sequence represents a fragment of the TNF-BP described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 HPONNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour necrosis factor; ethylene glycol; pharmokinetic; adult respiratory distress syndrome; rheumatoid arthritis; septic shock; pulmonary fibrosis; spacer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                      DNA encoding TNF binding protein and TNF- receptor - used in tumour treatment and to understand mechanisms to TNF action.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brewer MT, Kohno T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 EKQNTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
Stratowa C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.7%; Score 200.5; DB 29.8%; Pred. No. 1.2e-07; ive 20; Mismatches 72
   Maurerfogy I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evans RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR27496 standard; protein; 161 AA.
                                                                                                                                                                                                                         Claim 23; Page 34; 51pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91US-00669862.
92US-00822296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Native 30 kD TNF inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Conservative
Himmler A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Armes LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SYND ) SYNERGEN INC
                                                           WPI; 1990-321987/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-348933/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 161 AA;
   Hauptmann R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9216221-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 GOVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                         The sequence shows a native 30 kD TNF inhibitor which may be modified to contain at least one non-native cysteine residue, pref. at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is joined to a non-peptidic polymer, pref. monomethoxy PEG via thio-ether bonds. Two such TNF inhibitor mols. may be linked via this non-peptidic spacer. The modified polypeptides show improved pharmokinetic properties, i.e. increased mol. wt. hence reduced clearance rate following s.c. or systemic administration, increased sol. of native TNF inhibitors, and reduced antigenicity. The polypeptides may be used for treatment of TNF mediated diseases such as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid arthritis, inflammatory bowel disease and septic shock. The same method may be applied to the interleukin-1 receptor antagonist IL-1ra. See also AAR27495. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                                                                                                                                                                                     11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69
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                                                                                                                                                                                                                                                                                                                                                21; Gaps
                                                                                                                                                                                                                                                                                                             17.7%; Score 200.5; DB 2; Length 161; 29.8%; Pred. No. 1.2e-07; Live 20; Mismatches 72; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; tumour necrosis factor; TNF; TNF receptor type I; inflammatory disease; leukaemia; TNF binding protein; anti-inflammatory drug; methotrexatess.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 EKQNTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      soluble tumour necrosis factor receptor type I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Edwards CK;
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Claim 54; Fig 2; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0032587P.
97US-0036355P.
97US-0039315P.
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                                                                                                                                                                                                                                                                                                                                                48; Conservative
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Best Local Similarity
Matches 48; Conserv
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                                                                                                                                                                                                                                                                                  Sequence 161 AA;
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07-FEB-1997
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                                                                                 receptor type I, used in the method of the invention involving the treatment of acute or chronic inflammatory disease such as leukaemia by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM
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                                                           This is the amino acid sequence of the human tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                     DB 2; Length 161;
                                                                                                                                                                                                                                                                                              17.7%; Score 200.5; DB 2; Length 1
29.8%; Pred. No. 1.2e-07;
tive 20; Mismatches 72; Indels
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Job time : 164 secs
Disclosure; Fig 1; 104pp; English.
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 29.88
Matches 48; Conservative
                                                                                                                                                                                                                                         Sequence 161 AA;
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Sequence 430, App Sequence 16, Appl Sequence 11, Appl Sequence 11, Appl Sequence 19, Appl Sequence 21, Appl Sequence 21, Appl Sequence 429, Appl

Sequence 423, App

Sequence 3, Appli Sequence 4, Appli Sequence 12, Appl Sequence 3, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 53, Appl

14 US-10-218-102-423 14 US-10-218-102-430 9 US-09-899-429A-10 9 US-09-899-429A-11 14 US-10-218-102-421 15 US-09-798-789-11 16 US-09-798-789-13 17 US-09-798-789-13 18 US-09-708-789-13 19 US-09-708-789-13 10 US-09-808-12 15 US-10-808-12 15 US-10-808-12 16 US-10-632-929-12 17 US-10-632-929-12 18 US-10-632-929-12 19 US-09-809-234-4 10 US-09-809-234-4 11 US-10-436-826-73 12 US-10-436-826-73 13 US-10-436-826-73 14 US-10-436-826-73 15 US-10-496-238-2

Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 1, Appli Sequence 9, Appli Sequence 6, Appli

US-10-218-102-419 US-10-218-102-424 US-10-218-102-432

ALIGNMENTS

US-09-798-789-9 US-09-798-789-14 US-09-798-789-22 US-09-899-429A-6

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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION NUMBER: US/09/884,733 FILING DATE: 19-Jun-2001

CLASSIFICATION: cUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-884-733-1
Sequence 1, Application US/09884733
Sequence 1, Application US/09884733
Sequence 1, Application US/09884733
Sequence 1, Application US/09884733
SETTLE OF INVENTION: Apolication TITLE OF INVENTION: Application TITLE OF INVENTION: Applicati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFRAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/304,003
FILING DATE: 14-JUNE-2000
ATTORNEY/AGENT INFORMATION:
COUNTRY: USA
Sequence 5, Appli
Sequence 12, Appl
Sequence 422, App
Sequence 18, Appl
Sequence 13, Appl
Sequence 20, Appl
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Sequence 1, Appli
                                                                                                                             June 27, 2005, 14:02:25 ; Search time 162 Seconds (without alignments) 462.882 Million cell updates/sec
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1 MEQRPRGCAAVAAALLLVLL......CVSCPTSTLGSCPERCAAVC 195
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| cgn2_6/ptodata1/pubpaa/USO7_PUBCOMB.ppp:*
| cgn2_6/ptodata1/pubpaa/USO6_PUBCOMB.ppp:*
| cgn2_6/ptodata1/pubpaa/USO6_PUBCOMB.ppp:*
| cgn2_6/ptodata1/pubpaa/USO7_NEW_PUB.ppp:*
| cgn2_6/ptodata1/pubpaa/USO7_NEW_PUB.ppp:*
| cgn2_6/ptodata1/pubpaa/USO8_PUBCOMB.ppp:*
| cgn2_6/ptodata1/pubpaa/USO8_PUBCOMB.ppp:*
| cgn2_6/ptodata1/pubpaa/USO8_PUBCOMB.ppp:*
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| cgn2_6/ptodata1/pubpaa/USO9_PUBCOMB.ppp:*
| cgn2_6/ptodata1/pubpaa/USO0P_PUBCOMB.ppp:*
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-993-234-1
3 US-10-081-280-1
4 US-10-112-793-1
5 US-10-112-193-1
5 US-10-42-247-5
US-09-798-789-12
US-09-899-4284-18
US-09-798-789-13
US-09-798-789-13
US-09-798-789-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                            - protein search, using sw model
                                                                                                                                                                                                               US-10-081-280-6_COPY_1_195
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Maximum DB seq length: 195
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Match 1
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111:
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20:
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210.5
200.5
209.5
208.5
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                                                                                                                                    Run on:
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                 61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKFG 120
                                                                                                                                                                                                                                                                                                                                                                                                     121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                      1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP 60
                                                                                                                                                                                                                                                  1 MEORPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                     93.0%; Score 1051; DB 9; Length 181; 100.0%; Pred. No. 5.8e-76; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/993, 234
FILING DATE: 19-No. US20020146768A1-2001
CLASSIFTCATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
                                                                                                                ; SEQUENCE DESCRIPTION; SEQ ID NO: 1:
US-09-884-733-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/828,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: Linear SEQ ID NO: US-09-993-234-1
                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
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Patent No. US20020146768A1
GENERAL INFORMATION:
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TYPE: Amino Acid
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ATTORNEY/AGENT INFORMATION:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID 00: 1:
SEQUENCE CHARACTERISTICS:
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                TOPOLOGY: Linear
                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                           Similarity
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                                                                                                                                   1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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                                                                                                    1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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     Length 181;
                                                  Indels
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Publication No. US20020165157A1
GENERAL INFORMATION:
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
93.0%; Score 1051; DB 9;
100.0%; Pred. No. 5.8e-76;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Preu. ...
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P1007R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 181 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415/952-9881
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear
                                                  Matches 181; Conservative
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61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1051; DB 14;
Pred. No. 5.8e-76;
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100.0%; Pred. No.
                                                                                                                                                                         Sequence 1, Application US/10112193
Publication No. US20030004313A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/928,069
FILING DATE: 11-56P-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-56P-1996
ATTORNEY/AGENT INFORMATION:
NAME: MARESHARD DATE: 15.600
REFERENCE/DOCKET NUMBER: 91052R1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,193
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
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SEQUENCE CHARACTERISTICS
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Matches 181; Conservative
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US-10-415-247-5
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Best Local
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121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
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                                                                                            121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                     121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
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                                                                                                                                                                                                                                                                                                                                                                          APPLICANT ASHKenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSE:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIPICATION: CURKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 100.0%; Score 1051; DB 13; Similarity 100.0%; Pred. No. 5.8e-76; 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/828,683A FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328 FILING DATE: 1-AP-1996
APPLICATION NUMBER: 08/710802 FILING DATE: 2-Sep-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10112793
Publication No. US20020192729A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 181 amino acids
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SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
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Matches 181; Conservative
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100 SQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDC--GALHRHTRLLCSR 157
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                                                                                                                                          12 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASE-EHKRECLRCSRCRDKM 70
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                                                                                                       40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GABLICANT: Bentzien, Joerg
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Designaliais, John R.
APPLICANT: Designaliais, John R.
APPLICANT: Designaliais, John R.
APPLICANT: Vielmetter, Jost
TILE OF INVENTION: Procein Design Automation for Protein Libraries
FILE REPERBNCE: A-67229-11/RFT/RMS/RMK
CURRENT FILING DATE: 2002-08-12
FRICR APPLICATION NUMBER: US 60/927,790
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-09-15
PRIOR FILING DATE: 2001-09-15
PRIOR PLING DATE: 2001-09-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 432
SOFTWARE: Patentin version 3.1
                                                   Gaps
                                                 19;
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                                                 Indels
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                                                                                                                                                                                                                                                                                                                                158 RDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                 122 KONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 RDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
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                    Best Local Similarity 30.0%; Pred. No. 3.4e-09; Matches 48; Conservative 20; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .4e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 422, Application US/10218102; Publication No. US20030130827A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-899-429A-18
; Sequence 18, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 5, Application US/10415247

Publication No. US20040013655A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION:

GENOME responsible for chronic rheumatoid arthritis,

TITLE OF INVENTION:

Genome responsible for chronic rheumatoid arthritis and information and information arthritis, and therapeutic method and medicine of INTEL OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

APPLICATION NUMBER: US/10/415,247

CURRENT APPLICATION NUMBER: US/244

PRIOR APPLICATION NUMBER: UP 2000-324296

PRIOR APPLICATION NUMBER: UP 2000-324296

PRIOR APPLICATION NUMBER: UP 2001-90546

PRIOR FILING DATE: 2001-3.2

PRIOR FILING DATE: 2001-3.2

PRIOR FILING DATE: 2001-3.2

NUMBER OF SEQ ID NOS: 21

SEQ ID NOS: 21

SEQ ID NOS: 21
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Fatent No. US2002000978041

GENERAL INFORMATION:

APPLICANT: Dahiyat, Bassil

APPLICANT: Filikov, Anton

TITLE OF INVENTION: DISCOVERY OF PROTEIN BASED TNF-ALPHA

TITLE OF INVENTION: DISCOVERS

TITLE OF INVENTION WIMBER: US 60/186,427

PRIOR FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.0%; Score 1051; DB 15;
100.0%; Pred. No. 5.9e-76;
tive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 181
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US-10-218-102-423
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FEATURE:
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              APPLICANT: Anumeter, Copy, Ingrid
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: Them
FILE REPERBENCE: 99.385-J
CURRENT APPLICATION NUMBER: 09/792,356
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 1955-06-07
PRIOR FILING DATE: 1955-06-07
PRIOR PLING DATE: 1955-06-07
PRIOR PLING DATE: 1955-06-07
PRIOR FILING DATE: 1955-06-07
PRIOR FILING DATE: 1995-01-02
PRIOR FILING DATE: 1995-01-02
PRIOR FILING DATE: 1995-01-02
PRIOR FILING DATE: 1995-04-20
PRIOR FILING DATE: 1990-04-20
PRIOR FILING DATE: 1900-04-20
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Fatent No. US20020009780A1
GENERAL INFORMATION:
APPLICANT: Dahiyat, Bassil
APPLICANT: Pilikov, Anton
TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TWF-ALPHA
TITLE OF INVENTION: USATANTS FOR THE TREATMENT OF TNF-ALPHA
TITLE OF INVENTION: DISCORDER;
TITLE OF INVENTION: USO090-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/798,789
CURRENT FILING DATE: 2001-03-02
FRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 162
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US-09-899-429A-18
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ORGANISM: Artificial Sequence
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Himmler, Adolph
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71 GQVEISSCTVDRDTVCGCRKNQYRHYQSENLFQC----FNCSLCLN-GTVH----LSCQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-DCLQCSQCKKHD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
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                                                                                                                                                                                                                                                                                                                             Gaps
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CURRENT APPLICATION NUMBER: US/09/799, 789
PRIOR APPLICATION NUMBER: US 60/186,427
PRIOR PLLING DATE: 2000-03-02
SOFTWARE: PATCHIN UVE: 2.1
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-13
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18.2%; Score 205.5; DB 9; Length 162;
Best Local Similarity 30.4%; Pred. No. 8.5e-09;
Matches 49; Conservative 20; Mismatches 71; Indels 21;
                                                                                                                                                                                                   DB 9; Length 162;
                                                                                                                                                                                            Query Match 18.2%; Score 205.5; DB 9; Length 1 Best Local Similarity 30.0%; Pred. No. 8.5e-09; Matches 48; Conservative 19; Mismatches 74; Indels
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| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 RDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 423, Application US/10218102
Publication No. US20030130827A1
GENERAL INFORMATION:
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Patent No. US2002009780A1
GENERAL INFORMATION:
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APPLICANT: Dahiyat, Bassil I.
APPLICANT: Desjarlais, John R.
APPLICANT: Hayes, Robert J.
APPLICANT: Vielmetter, Jost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Himmler, Adolph
APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: TWF Receptors, TWF Binding Proteins and DNAs Coding for
                                                                                                                                                                                                                                                                                                                                            71 GQVEISSCTVDRDTVCGCRKNQYRHYQSENLFQC----FNCSLCLN-GTVH----LSCQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 SGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 SSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE-- 189
                                                                                                                                                                                                                                                                                                     100 SQVALENCSAVADTRCGCKPGWFVECQ---VSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 QDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVEC---QVSQCV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                12 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLVPHLGDREK---RDSVCPQGKY1HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 LLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCP
                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description of Artificial Sequence: recombinant
TNF-BP sequence
                                                                                                                                21;
                                                                 18.2%; Score 205.5; DB 14; Length 162; 30.4%; Pred. No. 8.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 18.1%; Score 205; DB 9; Length 173; 1 Similarity 29.0%; Pred. No. 9.9e-09; 54; Conservative 23; Mismatches 85; Indels 2
                                                                                                                             71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TILLE REFERENCE: 98-385-0
CURRENT APPLICATION NUMBER: US/09/899,429A
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 09/792,356
PRIOR PRILIGATION NUMBER: 09/792,356
PRIOR PILING DATE: 2000-02-23
PRIOR PILING DATE: 1955-06-07
PRIOR PILING DATE: 1955-02-01
PRIOR PILING DATE: 1995-02-01
PRIOR PILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR PILING DATE: 1993-11-17
PRIOR PELING DATE: 1993-11-17
PRIOR PELING DATE: 1993-11-17
PRIOR PELING DATE: 1992-01-02
PRIOR PILING DATE: 1992-01-02
PRIOR PILING DATE: 1992-01-02
PRIOR PILING DATE: 1992-01-02
PRIOR PILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PATENTIN VOY: 2.0
                                                                                                                             20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-899-429A-16
; Sequence 16, Application US/09899429A
; Patent no. US20020169118A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                             49; Conservative
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Best Local Similarity
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                                                                                               Best Local Similarity
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              US-10-218-102-430
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                                                                       Query Match
                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bentzien, Joerg
APPLICANT: Bantzien, Joerg
APPLICANT: Bantzien, Joerg
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Danis, John R.
APPLICANT: Hayes, Robert J.
APPLICANT: Vielmetter, Jost
ITILE OF INVENTION: Protein Design Automation for Protein Libraries
FILE REFERENCE: A-67229-11/RFT/RNS/RMK
CURRENT APPLICATION NUMBER: US/10/218,102
FRIOR APPLICATION NUMBER: US 09/927,790
FRIOR PILING DATE: 2001-08-10
FRIOR FILING DATE: 2001-09-10
FRIOR PILING DATE: 2001-09-10
FRIOR PILING DATE: 2001-09-10
FRIOR APPLICATION NUMBER: US 60/311,545
FRIOR APPLICATION NUMBER: US 60/311,937
FRIOR APPLICATION NUMBER: US 60/351,937
FRIOR PILING DATE: 2002-01-25
FRIOR PELING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 432
SOFTWARE: PatentIn version 3.1
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries
; FLIER REFRENCE: A-6729-11/RFY/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 69/927,790
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,545
; PRIOR APPLICATION NUMBER: US 60/324,899
; PRIOR APPLICATION NUMBER: US 60/351,937
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/351,937
; PRIOR FILING DATE: 2002-01-25
; PRIOR FILING DATE: 2002-01-25
; NUMBER FOR SEQ ID NOS: 432
; SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.0%; Pred. No. 8.5e-09;
Matches 48; Conservative 19; Mismatches 74; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 RDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 KONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 430, Application US/10218102
Publication No. US20030130827A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: synthetic
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Matches
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| :| 162 ECTKLC 167

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OTHER INFORMATION: Description of Artificial Sequence: recombinant; OTHER INFORMATION: TNF-BP sequence
US-09-899-429A-10
                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
RESULT 15
US-09-899-429A-10
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75 QDTFLAWENHHNSECARCOACDEOASOVALENCSAVADTRCGCKPGWFVEC---QVSQCV 131 15 LLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCP 74 24; Gaps Query Match 18.1%; Score 205; DB 9; Length 183; Best Local Similarity 29.0%; Pred. No. 1e-08; Matches 54; Conservative 23; Mismatches 85; Indels g 셤 ò ò

190 RCAAVC 195

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162 ECTKLC 167

Search completed: June 27, 2005, 14:15:50 Job time : 165 secs

CHEST AND TO SENT COMMENTS.

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, Appl Appli Appli

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61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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                                                              Sequence
Sequence
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PATENT NO. 6462176

GENERAL INFORMATION:

APPLICANT ABAKEMAZI, Avi J.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

STREET: 1 DNA WAY

CITY: South San Francisco
STREET: 1 DNA WAY

CITY: South San Francisco
STREET: 1 DNA WAY

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winheatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,069

FILING DATE: 11-Sep-1997

CLASSIFICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION NUMBER: 90/226943

FILING DATE: 09/23/1996

ATTORNEY/AGENT INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRAX: 650/952-9881

INFORMATION POR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 181 amino acids

TYPE: Amino Acid
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Pred. No. 1.7e-89;
                          US-09-411-722-1

US-09-852-266A-1

US-08-477-347-14

US-08-477-347-14

US-08-477-347-14

US-08-476-862-5

US-08-806-803-15

US-09-800-909-5

US-09-800-909-14

US-09-180-100-9

US-09-180-100-15

US-08-868-848-4
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100.0%; Pred. No. 1...
0; Mismatches
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Sequence 1, Appli
Sequence 4, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                       1 MEQRPRGCAAVAAALLLVLL......CVSCPTSTLGSCPERCAAVC 195
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. /cgn2 6/ptodata1/iaa/6B_COMB.pep:*
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Compugen Ltd.
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US-08-468-660-4

US-09-800-908-12

US-09-800-908-12

US-09-813-33-32-53

US-09-328-683A-12

US-09-328-683A-12

US-09-328-683A-12

US-09-328-683A-12

US-09-146-250-129

US-09-146-950-2

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                          GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 protein search, using sw model
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Match Length DB
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Maximum DB seq length: 195
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Perfect score:
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STREET: P.O. Box CITY: Arlington STATE: Virginia COUNTRY: USA
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                           181 T 181
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61 CTEPCGNSTCLVCPQDTFLAWENHINSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                   121 WFVECOVSOCVSSSPFYCOPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                          121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
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                                                                                                                                                                                                                                                                                 US-08-828-683A-1

Sequence 1, Application US/08828683A

Patent No. 6469144

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Geneticch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION TUMBER: 08/52328
FILING DATE: 1-AQP-1996
APPLICATION NUMBER: 08/710802
APPLICATION NUMBER: 08/710802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: I DNA Way
CITY: South San Francisco
STATE: California
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TYPE: Amino Acid
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INFORMATION FOR SEQ ID NO: 1:
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Matches 181; Conservative
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Sequence 4, Application US/08219237B
Patent NO. 5874546
GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: TOH, Naoto
APPLICANT: VONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: 11
CORRESPONDENCES: Jees W. Hellwege
ADDRESSEE: Jees No. Box 2266 Eads Station
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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ZIP: 22202

COMPUTER READABLE FORM:
MEDITUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.25
SOFFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/219,2378
FILING DATE: 28-MRA-1994
CLASSIFICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: James W Hellwege
REGISTRATION NUMBER: 28,808
REGISTRATION NUMBER: 216762
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TENGTH 153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08477347
Patent No. 6232446
SENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
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amino acid
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MOLECULE TYPE: protein
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100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
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APPLICANT: NAGATA, Shigekazu
APPLICANT: TOW, Naoto
APPLICANT: TOWERARA, Shin
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE;
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STREET: P.O. BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.7%; Score 200.5; DB 3; Length 29.8%; Pred. No. 3.5e-11; tive 20; Mismatches 72; Indels
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                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION UNDATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: WALLACH=12A TELECOMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                       FILING DATE: 07-JUN-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION NUMBER: IL 91229
FILING DATE: 06-APR-1990
PRIOR APPLICATION NUMBER: IL 91229
FILING DATE: 18-MAY-1989
APPLICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 48; Conserva
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    D.C.
                                              20004
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                                                                                                                                                   ZIE: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
17.7%; Score 200.5; DB 3;
Best Local Similarity 29.8%; Pred. No. 3.5e-11;
Matches 48; Conservative 20; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION DATA:
FILING DATE:
PRIOR APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, G. KEVIN
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACTELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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Patent No. 626239
GENERAL INFORMATION:
APPLICANT: BELETKY, IGOR
APPLICANT: BELETKY, IGOR
APPLICANT: METT, IGOR
APPLICANT: METT, IGOR
APPLICANT: METT, IGOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SEVENTH Street, N.W.
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419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/115,685
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TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
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amino acid
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NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
                                                                                         Washington
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                                                                                                         STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-477-347-12
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US-08-476-862-3
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21; Gaps

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APPLICATION NUMBER: US/09/800,908
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ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
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APPLICANT: WALLACH, David BIGDA, Jacek BELETSKY, Igor METT, Igor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 08-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
FILING DATE: 06-AUG-1989
FILING DATE: 06-AUG-1989
FILING DATE: 18-MAY-1989
APPLICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989
ATTONNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET I.
REGISTATION NUMBER: 25,618
REGISTATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 35,618
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
APPLICATION NUMBER: 08/476,862 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERLETICS: LENGTH: 153 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 29.8%
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
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                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,560C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGRAT INFORMATION:
NAME: MURPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
RESERENCE/DOCKET NUMBER: 20-4393P
TELEPRANICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/09/800,909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
APPLICANT: BNGELWANN, Hartmut
TITLE OF INVENTION: TNF INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 419 Seventh Street, N.W. CITY: Washington
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09800909
Patent No. 6555111
GENERAL INFORMATION:
APPLICANT: WALLACH, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 703-205-8000
TELEPAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 153 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CLASSIFICATION:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20004
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         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-800-909-3
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100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                                                      68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                               40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                       9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                      Gaps
                                                                      21;
      DB 4; Length 153;
17.7%; Score 200.5; DB 4; Length 1
29.8%; Pred. No. 3.5e-11;
Live 20; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          157 RRDIDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
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APPLICATION NUMBER: 08/477,347
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100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                                                                                                                                                                                                                                                           9 HPONNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                              40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                       Query Match 17.7%; Score 200.5; DB 4; Length Best Local Similarity 29.8%; Pred. No. 3.5e-11; Matches 48; Conservative 20; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                            TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-08-828-683A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 53, Application US/09523323
Patent No. 6635743
                                                                                     LENGTH: 154 amino acids TYPE: Amino Acid
             TELEFAX: 650/952-9881
                                  INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 53 LENGTH: 154 TYPE: PRT
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APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-523-323-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 153;
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TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genettech, Inc.
STREET: 1 DNA WAY
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FILING DATE: <Unknown>
APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSENT G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH=10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 17.7%; Score 200.5; DB 4
Best Local Similarity 29.8%; Pred. No. 3.5e-11;
Matches 48; Conservative 20; Mismatches 72
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APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 35,600
REGERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-800-908-12
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FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08828683A Patent No. 6469144 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                      LENGTH: 153 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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APPLICANT: KIDEN, Stephen M.
APPLICANT: ENDAY, Yifan
APPLICANT: Chai, Yifan
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
TILE REPRENCE: 1488.065000C
CURRENT PILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 60/168,380
EARLIER PILING DATE: 1999-12-02
EARLIER PILING DATE: 1999-03-10
EARLIER PILING DATE: 1999-00-10
EARLIER PILING DATE: 1999-00-03-06
EARLIER PILING DATE: 1999-03-11
EARLIER PILING DATE: 1999-03-11
EARLIER PELICATION NUMBER: 60/124,041
EARLIER APPLICATION NUMBER: 60/124,041
EARLIER PILING DATE: 1999-03-11
EARLIER PELING DATE: 1999-03-11
EARLIER PELING DATE: 1999-03-11
EARLIER PELING DATE: 1999-03-13
EARLIER PELING DATE: 1999-03-13
EARLIER PELING DATE: 1999-03-13
EARLIER PELING DATE: 1999-03-14
EARLIER PELING DATE: 1999-03-15
EARLIER PELING DATE: 1999-03-16
EARLIER PELING DATE: 1999-03-17
EARLIER PELING DATE: 1999-03-03-18
EARLIER PILING DATE: 1999-03-17
EARLIER PILING DATE: 1999-03-17
EARLIER PILING DATE: 1999-03-17
EARLIER PILING DATE: 1999-03-17
EARLIER PILING DATE: 1999-03-18
EARLIER PELING DATE: 1999-
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100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                             70 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
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  11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCDECESQSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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                                                                                                                                        157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                  157 RRDIDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CONTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/23,087A FILING DATE: 08-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1..154
OTHER INFORMATION: /note= "TNFR1, see Fig. 5"
                                                                                                                                                                                                                                                                       US-08-232-087A-10
; Sequence 10, Application US/08232087A
; Patent No. 5866372
; GENERAL INFORMATION:
    APPLICANT: Stein, Harald
    APPLICANT: Latza, Ute
    APPLICANT: Latza, Ute
    TITLE OF INVENTION: Lymphoid CD30-Antigen
    NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22042
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Paint.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 756-103P
TELECOMONINICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 30.44
Matches 49; Conservative
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STATE: Virginia
COUNTRY: U.S.A.
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LOCATION: 1..154
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                         7;
                                                                                                                                                           100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                        68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                    40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
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                         21; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09326394

Patent No. 6306820
GENERAL INFORMATION:
APPLICANT: Bendele, Alison M.
APPLICANT: Sennello, Regina M.
APPLICANT: Genards, Carl K.
TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES
NUMBER OF SEQUENCES:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
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                         Indels
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                                                                                                                                                                                                                                                  157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                   Query Match 17.7%; Score 200.5; DB 3; Best Local Similarity 29.8%; Pred. No. 3.7e-11; Matches 48; Conservative 20; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
nilarity 29.8%; Pred. No. 3.5e-11; Conservative 20; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICATION DATA:
APPLICATION NUMBER: US 60/032,587
FILING DATE: 06-DEC-1996
PRICATION NUMBER: US 60/036,355
FILING DATE: 23-07M-1997
PRICATION NUMBER: US 60/039,315
PRICATION NUMBER: US 60/039,315
FILING DATE: 07-FEB-1997
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 60/052,023
FILING DATE: 09-UL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Zindrick, Thomas K.
REGISTRATION NUMBER: 32,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/326,394
FILING DATE: 08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A-430D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1840 DeHavilland Drive CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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Best Local Similarity
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                         48;
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-146-950-2
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LENGTH: 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Taylor, J. Michael
APPLICANT: Kehrli, Jr., Marcus
APPLICANT: Lee, Eun-Kyung
APPLICANT: Lee, Eun-Kyung
APPLICANT: Lee, Eun-Kyung
APPLICANT: Lee, Tun-Kyung
APPLICANT: Lee, Tun-Kyung
APPLICANT: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
ITILE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
ITILE OF INVENTION: BOVINE TUMOR NETHORS OF USE
FILE REFERENCE: 08411-018001
CURRENT APPLICATION NUMBER: US/09/513,007
CURRENT APPLICATION NUMBER: 60/122,156
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.3%; Score 196; DB 3; Length 139; 31.5%; Pred. No. 8.2e-11; Live 17; Mismatches 67; Indels
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119 KQNTVC-TCHAGFPLRENECVSC----GNCKKSLECTKLC 153
                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Boyle, William
APPLICANT: Lacey, David
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT PILING DATE: 1996-09-03
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR PILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patentin version 3.1
SEQ ID NO 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 RRDTDCGTCLPGFYEHGDGCVSC 179
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                                                                                                                            Sequence 129, Application US/08706945D Patent No. 6369027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09513007
Patent No. 6406907
GENERAL INFORMATION:
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Best Local Similarity 31.5%
Conservative
Conservative
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; ORGANISM: Homo sapiens
US-08-706-945D-129
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Best Local Similarity
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DD 22 HPOWSTICCTRCHKGTTLINDCPGRADDCRVCAPGTTALEWHLR.—E.15 |
DD 30 PALENGTYBERGORDSPERVCAPGTTALEWHLR.—E.16 |
DD 310 SGVALLASANATRCGRCKGRAN-CA-OTTALEWHLR.—E.16 |
DD 312 REDDGGCTCLEGFYBHGDGCVSCFTSGTGCRCLMCSLCDRGTWN---IPCQE 131 |
DD 132 RGDTIC-HCHMGFFLKGARKTISCHDCGWSCFEKLC 165 |
RESULT 15
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Oresul Mina in Jung 28/47

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2005
           Copyright
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- protein search, using sw model OM protein

Run on:

June 27, 2005, 14:04:00 ; Search time 38 Seconds (without alignments) 440.571 Million cell updates/sec

1 QGGTRSPRCDCAGDFHKKIG......CPTSTLGSCPERCAAVCGWR 174 US-10-081-280-6_COPY_25_198 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

87400 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 174 Minimum DB Maximum DB

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	ultra high-sulfur	trophozoite surfac	Fas-Delta-(4,7) pr	metallothionein-2		cysteine-rich hair	ferredoxin-type pr	hair keratin cyste	finger protein (cl	keratin high-sulfu	high-sulfur wool m	cellular nucleic a	zinc finger protei	cellular nucleic a	hypothetical prote		hypothetical prote	_	S	hypothetical prote	_			hypothetical prote	_	probable metalloth	igh	high-sulfur wool m	vasotocin 2 / neur
	ID	S18946	PC1294	S58662	S50911	B21761	146489	AG0369	S60314	806570	KRGT3M	147108	148298	A55499	148297	T20467	KRSH3A	T24272	F65072	G65156	T25185	F86032	H91185	B82430	T20463	D37057	E83378	KRSHHC	71	B32669
	DB		~	~	N	~	~	-4	~	~	-	0	~	~	0	N	-	~	~	~	~	7	~	~	N	~	7	-	~	7
	Length	169	141	149	104	143	126	167	151	168	131	152	171	170	170	133	130	164	163	157	160	157	157	168	132	92	79	152	152	155
Ouerv	- '	9.6	9.3	9.5		9.0			•	8.1								7.9					٠	7.7	٠	٠	7.5			7.5
	Score	103	96.5	96	94.5	3	90	88	98	4	83.5	m	ന	83	83	82.5	82	81.5	0	80	80	σ	79.5	σ	79	78.5	78	78	78	78
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metallothionein 3 metallothionein-II	keratin high-sulfu	metallothionein II	probable oxidoredu	probable oxidoredu	hypothetical prote	NapF Ferredoxin co	metallothionein-li	metallothionein II	electron transport	finger protein (cl	growth inhibitory	metallothionein 3,	high-cysteine chor	probable oxidoredu
S44392 T07090	KRGT3J	JC6521	F91098	B85944	T15610	D95346	A55011	T05719	H75154	806557	167866	A46034	A21761	B83410
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8 8 22 82 83	132	68	131	131	135	166	69	82	166	168	68	89	124	153
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77.5	77	76.5	16	7	•	75					74	74	74	74

ALIGNMENTS

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J. Cell Biol. 111, 2587-2600, 1990
A;Title: Structure and expression of genes for a class of cysteine-rich proteins of the c
A;Reference number: A36686; MUID:91115951; PMID:1703541
A;Accession: B36686
                                                                                                                                                                                                                                                                                                                       A;Accession: S18946
A;Molecule type: mENA
A;Residues: 1-169 - ORA-
A;Cresidues: 1-169 - ORA-
A;Cresidues: UNIPROT:Q14564; EMBL:X63755; NID:g32471; PIDN:CAA45283.1; PID:g32472
R;MacKinnon, P.J.; Powell, B.C.; Rogers, G.E.
J. Cell Biol. 111, 2587-2600, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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                                                                  C;Species: Homo sapiens (man)
C;Accession: S18946; Bacdence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: S18946; Bacdence, D
Submitted to the EMBL Data Library, December 1991
A;Description: Nucleotide sequence of a Human high-sulphur keratin cDNA.
A;Reference number: S18946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 CCRGCPAGHYLKAPCTEPCG--NSTCLVCPQDTFLAWENHHNSECARCQ-----ACD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-39,'Y',41-169 <MAC>
A;Croserreferences: GB:X55293; NID:g34078; PIDN:CAA39005.1; PID:g34079
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
                                 N;Alternate names: UHS keratin; ultra high-sulfur matrix protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch '9.9%; Score 103; DB 1; Length 169; I Similarity 25.3%; Pred. No. 0.58; 45; Conservative 6; Mismatches 71; Indels !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Craice: Objection: 1013-1013
A;Map position: 11q13-11q13
C;Superfamily: ultra-high-sulfur keratin
C;Superfamily: ultra-high-sulfur keratin
C;Keyvords: hair; tandem repeat
F;1-15/Region: Ser-rich nonapeptide repeat
F;5-68/Region: Gly-rich decapeptide repeat
F;6-78/Region: Gly-rich decapeptide repeat
F;69-78/Region: Gly-rich decapeptide repeat
F;89-97/Region: Cys-rich decapeptide repeat
F;89-97/Region: Cys-rich decapeptide repeat
F;108-117/Region: Cys-rich decapeptide repeat
F;108-117/Region: Cys-rich decapeptide repeat
F;118-126/Region: Ser-rich nonapeptide repeat
F;118-126/Region: Cys-rich decapeptide repeat
F;137-145/Region: Cys-rich decapeptide repeat
F;156-165/Region: Cys-rich decapeptide repeat
F;156-165/Region: Cys-rich decapeptide repeat
F;156-165/Region: Cys-rich decapeptide repeat
ultra high-sulfur keratin 1 - human
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Best Local S:
Matches 45
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R,Iatrou, K.; Tsitilou, S.G.; Kafatos, F.C.
Proc. Natl. Acad. Sci. U.S.A. 81, 4452-4456, 1984
A;Title: DNA sequence transfer between two high-cysteine chorion gene families in the sil A;Reference number: A21761; MUID:84272653; PMID:6589605
A;Accession: B21761
A;Katus: preliminary
A;Molecule type: DNA
A;Residues: 1-143 <1AT>
C;Superfamily: chorion class A protein pc292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 ENHINSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 ENRYKGDVC----VCGEVPFLGTADVCGNMCSSGCGCID-----YGCGNGCVGITRSC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGTGEGCKCTGCKCCQPAKSGCCCGDKAKACCTDP--NSGC-CCSKTNKCCDSTNKTE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 CDCAGDFHKKIGLFCCR----GCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 CGC------CCRGCGCG-----CGGCGCCCENFRVCSNSAAPIGLSICS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        high cysteine chorion B 12 protein precursor - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cysteine-rich hair keratin associated protein - rabbit
C;Species: Oryccolagus cuniculus (domestic rabbit)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I46489; S49201
GQPCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GCGGC-----GCGCGGC-----GCCGCSCGRSC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPERCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 94.5; DB 2; Length 104; Pred. No. 1.8; 8; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVC----
                                                                                                                                                                                                  metallothionein-2 - Tetrahymena pigmentosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity 34.3%;
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 GGCGC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 CARCOAC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Genetic code: SGC5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Si
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Si
Matches 36
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                                                                                                                                                                                                                                                                                                                                              trophosoite surface antigen - Giardia lamblia (strain Adelaide-1) (fragment)
C;Species: Giardia lamblia
C;Species: Giardia lamblia
C;Species: Giardia lamblia
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: PCi294
R;Ey, P.L.; Mayrhofer, G.
Gene 129, 257-262, 1993
A;Title: Two genes encoding homologous 70-kDa surface proteins are present within indivi
A;Reference number: PCI294; MUID:93314970; PMID:8325510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fas-Delta-(4,7) protein - human (5/8662)
Fas-Delta-(4,7) protein - human (5/8662)
C/Species: Homo sapiens (man)
C/Decies: Homo sapiens (man)
C/Decies: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: 858662; 857566
R/Liu, C.; Cheng, J.; Mountz, J.D.
R/Liu, C.; Cheng, J.; Mountz, J.D.
A/Title: Differential expression of human Fas mRNA species upon peripheral blood mononuc A/Reference number: 858662; MUID:96013198; PMID:7575433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 CYETVKYPGKTV-----CISAPNGGTCQKAADGYKLDSGTLTVCSEGCKECTSSTDCTT 110
PVCCCVPACSCSSCGKRGCGSCGGSKGGCGSCGCSQCSCCKPCCCSSGCGSSCCQCSC-- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
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                                                                              125 RHTRLLCSRRDTDCGTCLPGFYEHGDG---CVS-----CPTSTLGS--CPERCAAVC 171
                                                                                                                                                        -----CKPYCSQCSCCKPCCSSSGRGSSCCQSSCCKPCCSSSGCGSSCCQSSCCKPC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GASYCSECATIT----EYPQNGVCAPKASRATPICNDSPIQNGV--CGICADNYFKNNGG
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C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 GLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDE
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A;Residues: 1-149 <LIU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.2%; Score 96; DB 2; Length 149; Best Local Similarity 33.3%; Pred. No. 1.7; Matches 18; Conservative 7; Mismatches 29; Indels
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A;Molecule type: mRNA
A;Residues: 1-132 «SCH»
A;Cross-references: EMBL;X89101; NID:g887457; PID:g887458
C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 CLPGFYEHGDGCVSCPTS--TLGSCPERCAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Schatzlein, C.E. BNIPROT:P25445 R;Schatzlein, C.E. Bubmitted to the EMBL Data Library, June 1995 A;Reference number: 857565 A;Accession: 857566 A;Status: nr.1'
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C;Keywords: surface antigen
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A;Residues: 1-141 <EYP>
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C;Accession: S06570 Roughell, H.; Pieler, T.; Koester, M.; Poeting, A.; Knoeche A;Nietfeld, W.; Bl-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeting, A.; Knoeche A;Title: Second-order repeats in Kenopus laevis finger proteins.
A;Reference number: S05632; MUID:90040698; PMID:2509712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NiAlternate names: MZ.6 procein
C;Species: Capra aegagrus hircus (domestic goat)
C;Species: Capra aegagrus hircus (domestic goat)
C;Accession: B92978; A02840
R;Joubert, F.J.
J. S. Afr. Chem. Inst. 28, 250-263, 1975
A;Title: Studies on the high-sulphur proteins of reduced mohair. The isolation and the an
C;Accession: S60314

R;Fratini, A.; Powell, B.C.; Hynd, P.I.; Keough, R.A.; Rogers, G.E.

J. Invest. Dermatol. 102, 178-185, 1994

J. Reference number: S60314; MUID:94149288; PMID:7508963

A;Reference number: S60314; MUID:94149288; PMID:7508963

A;Retus: preliminary

A;Redidue: 1-151 - FRA>

A;Residues: 1-151 - FRA>

A;Cross-references: UNIPROT:Q28576; EMBL:X73462; NID:G512030; PIDN:CAA51841.1; PID:G51203: C;Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 CICSECGKSFTDHAGLRIHQKYHTGVKPFSCSECGKCFTRRS----GLTAHLRIHTGEK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 ALENCSAVADTRCGCKPGWFVECQVSQCVSS--SPFYCQP--CLDCGALHRHTRLLCSRR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 CGNSTCLVCPQD--TFLAWENHHNS----ECARCOACDEQASQVALENCSAVADTRCGCK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       finger protein (clone XlcGF42-1) - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GEKPYSCSDCGKCFTRRWNLSEHRKSHTGQKRFCCSVCGKGFSYHSQMKSHYRTHTGEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCR-GCPAGHYLKAPCTEP-CGNSTCL--VCPQDTFLAWENHHNSECARCQACDEQASQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 CCRPSCCQTTCCRTTCYRPSCGVSSCRPICCQPT-----CPRPTCC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYTCTEC--GKC----FTCRT-----DLARHLRIHTENKPFTCSQCEKSFASHSD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                        ch 8.3%; Score 86; DB 2; Length 151; 1 Similarity 24.8%; Pred. No. 9.4; 38; Conservative 14; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 8.1%; Score 84.5; DB 2; Length 1 Similarity 23.3%; Pred. No. 13; 41; Conservative 13; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 PSCCGSSC----YRPSCCLRPVCNRVSCHTTC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 DIDCGICLPGFYEHGDGCVSCPISILGSCPERC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: not compared with conceptual translation
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A;Cross-references: UNIPROT:P18720
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GTRSPRC-DCAGDFHKKIGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local &
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Matches 3
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                                                                                                                                                                                                                                      A;Residues: 1-126 <POW>
A;Cross-references: UNIPROT:Q28707; EMBL:X80035; NID:g510540; PIDN:CAA56339.1; PID:g5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferredoxin-type protein NapF [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG0369
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; II, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: Ab0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Cross-references: UNIPROT: Q8ZCF1; GB: AL590842; PIDN: CAC92282.1; PID: 915980993; GSPDB: G
   R,Powell, B.C.; Arthur, J.; Nesci, A.
Differentiation 58, 227-232, 1995
A;Title: Characterization of a gene encoding a cysteine-rich keratin associated protein
A;Reference number: 146489; MUID:95228955; PMID:7536172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 QACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 -FTSVEQT-----AWQIKASISDRCLPYNQVECRSCQDSC----ETRAIKFRPRLSGI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
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S60314
S60314
Cistatin cysteine rich protein - sheep
Cispecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cispecies: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 CGQDFCQEES----CRPSC----CRPQCCQPSCCRPTCCI-----SSCCRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 CAGDFHKKIGLFCCR-GCPAGHYLKAPCTEP-CGNSTCLVCPQDTFLAWENHHNSECARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 NCSAVADTRCGCKPGWFVECQVS-QCVSSSPFYCQPCLD-CGALHRHTRLLCSR----
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C;Superfamily: ferredoxin protein NapF; ferredoxin 2[4Fe-4S] homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 QCCQ-----SVCCQPTC-CRP----SCYISSC--CRPTCCRP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 LLCSR----RDTDCGT-----CLPGFYEHGDGCVS--C-PTSTLGSC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 -rccrprccrprscorrccrroccrpsc----cvsrccrpccssdsc 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.5%; Score 88; DB 1; Length 167; Best Local Similarity 23.2%; Pred. No. 7.1; Matches 36; Conservative 18; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 ------RDTDCGTCLPGFYEHGDGCVSCPTSTL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQPELDLPACTGCGACVPG------CPVQAV 158
                                                                                                                             A,Accession: 146489
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                             8.7%; Score 90; DB 2
25.4%; Pred. No. 4.3;
tive 9; Mismatches
                                                                                                                                                                                                                                                                                                C,Genetics:
A,Gene: KAP4L
C,Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-167 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: AG0369
A; Status: preliminary
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A,Title: Mouse cellular nucleic acid binding proteins: a highly conserved family identifi A,Reference number: A55499; MUID:95203870; PMID:7896269
A,Accession:148298
A,Status: preliminary; translated from GB/EWBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-171 - REES>
A,Cross-references: UNIPROT:P53996; EMBL:211871; NID:950474; PIDN:CAA77897.1; PID:950475
C,Superfamily: cellular nucleic acid-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Accession: A55499
R;Warden, C.H.; Krisans, S.K.; Purcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; Te Genomics 24, 14-19, 1994
A;Title: Mouse cellular nucleic acid binding proteins: a highly conserved family identif; A;Reference number: A55499; MUID:95203870; PMID:7896269
A;Reference number: A55499
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cellular nucleic acid binding protein clone 6 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48297; S19861; S19959
R;Warden, C.H.; Krisans, S.K.; Purcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; Ts
Genomics 24, 14-19, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 NHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 HHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                RCGESGHLAKDCDLQEDEACYNCGRGGHIAKDCKEPKREREQC----CYNCGKPDHLARD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 DHADE-QKCYSCGEFGH--IQXDCTKVKCYRCG-ETGHV----AINCSKTSEVNCYRCGE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 RCDCAGDFHKKIGL--FCCRGCPAGHYLKAPCTEP----CGNSTCLVCPQDTFLAWEN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                            8 RCDCAGDFHKKIGL---FCCRGCPAGHYLKAPCTEP----CGNSTCLVCPQDTFLAWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:L12693; NID:g292347; PIDN:AAA89198.1; PID:g292348
                                                                                                                                                                                                                                                           Length 171;
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8.0%; Score 83; DB 2; Length 170;
Best Local Similarity 27.0%; Pred. No. 17;
Matches 34; Conservative 13; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                     59; Indels
                                                                                                                                                                                                                                                           ch 8.0%; Score 83.5; DB 2; Similarity 26.8%; Pred. No. 15; 34; Conservative 13; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Map position: 3q13.3-3q24
C,Superfamily: cellular nucleic acid-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zinc finger protein 9 - human
N;Alternate names: nucleic acid binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GDB:125342; OMIM:116955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DCGALHR 125
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157 ESGHLAR 163
                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 34; Conserva
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                                                                                                                                       A; Experimental source: Angora breed
C; Comment: Wool and hair consist of microfibrils embedded in a rigid matrix of other pro
C; Superfamily: keratin high-sulfur matrix protein IIIA
C; Keywords: duplication; hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reaidues: 1-152 <ROG>
A;Cross-references: UNIPROT:Q29620; GB:L33888; NID:g499874; PIDN:AAB01447.1; PID:g940358
C;Superfamily: keratin high-sulfur matrix protein IIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cellular nucleic acid binding protein clone 14 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 148298; S1996
R;Warden, C.H.; Krisans, S.K.; Purcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; Genomics 24, 14-19, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 CPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TTC--CQP-----VSVQCPCCRPTSCQPAPC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSAVADTRCGCKPGWFVECQV-----SQCVSSSPFYCQP------CL---- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 SSPFYCOPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSC-PERC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 COPTCLOTSGCKTGCGIGGSIGYGOVGSSGAVSSRTRWCRPDCRVEGTSLPPCCVVSCTS 104
                                                                                                                                                                                                                                                                                                                                                                                             2 GGTRSPRC---DCAGDFHKKIGLFCCRGCPAGHYLKAP-----CT----EPCGNSTCLV 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 GGCLQPRCYRDPC------CCRPVSCQTTVSRPVTFVSRCTRPICEPCRRPVC-- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 -----CRP---ITCCPTSC-- 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALEN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CCSTSFCGFPI-CPTAGTCGSSCC------RSTCSQTSCC--OPTSIQTSC 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 - DCGALHRHTRLLCSRRDTDCG--TCLPGFYEHGDGCVSCPTSTLGSCPERCA-AVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSCCQLYYAQASCC--RPSYCGQSCCRP----ACCCQPTCTEPVCBPTCSQPIC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: 147108
R;Rogers, G.R.; Hickford, J.G.; Bickerstaffe, R.
Anim. Genet. 25, 407-415, 1994
A;Title: Polymorphism in two genes for B2 high sulfur proteins of wool. A;Reference number: 147105; MUID:95209146; PMID:7695121
A;Accession: 147108
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                            91;
                                                                                                                                                                                                                                                                                  Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68; Indels
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                  Score 83.5; DI
Pred. No. 13;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
8.0%; Score 83.5; Di
Best Local Similarity 22.0%; Pred. No. 14;
Matches 39; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             high-sulfur wool matrix protein B2C - sheep
                                                                                                                Cross-references: UNIPROT: P02442
                                                                                                                                                                                                                                                                                     8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 -QAVVCRPC--CWA----
                                                                                                                                                                                                                                                                                                                                         42; Conservative
  A; Reference number: A92978
                    A Molecule type: protein
A, Residues: 1-131 < JOU'>
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 AAVC 171
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Matches
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Title: Mouse cellular nucleic acid binding proteins: a highly conserved family identif
Reference number: A55499; MUID:95203870; PMID:7896269
Accession: 148297
                                                                                                                                                                                   R;Warden, C.H.
submitted to the EMBL Data Library, January 1992
A;Description: Cellular nucleic acid binding protein (CNBP) is an extremely conserved cy
A;Accession: S19861
A;Accession: S19861
                                                                                                          A;Molecule type: mRNA
A;Residues: 1-170 <RES>
A;Cross-references: UNIPROT:P53996; EMBL:Z11870; NID:g50472; PIDN:CAA77896.1; PID:g50473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :cross-references: UNIPROT:09XVB0; EMBL:Z81493; PIDN:CAB0400.1; GSPDB:GN00020; CESP:F0; Experimental source: clone F01D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.9%; Score 82.5; DB 2; Length 133;
24.0%; Pred. No. 16;
tive 11; Mismatches 44; Indels 59; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 DHADE-QKCYSCGEFGH--IQKDCTKVKCYRCG-ETGHV----AINCSKTSEVNCYRCGE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 HHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 RCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPC-LDCGALHR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --AKQGYCTSCFLDCAEKIQ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 RCGESGHLAKDCDLQEDACYNCGRGGHIAKDCKEPKREREQC----CYNCGKPGHLARDC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 RCDCAGDFHKKIGL--FCCRGCPAGHYLKAPCTEP-----CGNSTCLVCPQDTFLAWEN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 PRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 PLADC----HAYAGL--CSNPMYTSFLDKYCPKTCG-----LCPDSTTL------ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ypochetical protein F01D5.2 - Caenorhabditis elegans
;Species: Caenorhabditis elegans
;Jate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-170 <WA2>
A;Cross-references: EMBL:X63866; NID:950470; PIDN:CAA45345.1; PID:950471
C;Superfamily: cellular nucleic acid-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, November 1996
A;Reference number: 219279
A;Accession: T20467
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-133 <WIL>
                                                                                 Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
8.0%; Score 83; DB 2
Best Local Similarity 27.0%; Pred. No. 17;
Matches 34; Conservative 13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 N----CAK---SCGFCNP-----EACLNC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: June 27, 2005, 14:19:24 Job time : 40 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.9%
Best Local Similarity 24.0%
Matches 36; Conservative
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A,Map position: 2
A,Introns: 81/2
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SEQUENCE
Query Match
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Matches
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AC Q8MJ
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bombyx mori
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cowpox viru
vaccinia vi
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human cytom
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human cytom
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Q8mj20 macaca mula
Q7zzy4 gallus gall
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07zzy4
08zg51
08sg51
09jke0
09bir3
09bir3
09bir3
08bdcs
07tfh9
08bdcs
06itv8
09dj12
07z761
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                    GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                             Fotal number of hits satisfying chosen parameters:
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QBUYL3
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Listing first 45 summaries
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1038
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Q911R0
Q6P2H9
Q8BDC6
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Q9DJL2
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Q8SQ52
Q8SQ51
Q9JKE0
Q8SQ49
Q9BIR2
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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length: 174
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Perfect score:
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                                                                                                                                               Run on:
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091913 xenopus lae
09738 tetrahymena
083022 rhodobacter
09rad6 rhodobacter
06y119 drosophila
061898 homo sapien
061899 homo sapien
09byr5 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mus musculu
                                         sapien
                                                         tetrahymena
                                                                           tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 KIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                       homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.9%; Score 165.5; DB 2; Length 150; 30.8%; Pred. No. 1.7e-06; tive 13; Mismatches 52; Indels 7
                 09d732
09byq4
P80394
                                                                           Q8t6b3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Careau R.R., Dharmarajan A.;

Labilted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

R Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

R HSSP; QQ2956; JUMA.

R GO; GO:0016020; C.membrane; IEA.

GO; GO:00004888; F:transmembrane receptor activity; IEA.

GO; GO:00006915; P:immune response; IEA.

R GO; GO:0007165; P:immune response; IEA.

R GO; GO:0007165; P:immune response; IEA.

R InterPro; IPR001369; TNFR_C6.

R PRINTS; PR01680; FASTRCEPTOR.

R PRMNTS; RR01680; FASTRCEPTOR.

R SMART; SM00208; TNFR, 2:

R PROSITE; PS00626; TNFR, 2:

R PROSITE; PS00626; TNFR_NGFR_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 EVETNCTRIQNTKCRCKENFY--CNASLC----DHCYHCTSCG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 VALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150
16644 MW; 7DEC76EC40A6BA4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                   150
0618F6
09D732
KR92 HWAN
MT1_TETF1
WT1_TETF7
0919J3
MT1_TETFY
0913D2
093D22
098AD6
0618G8
0618G8
0618G8
KR42_HWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8MJ20 PRELIMINARY; PRT; Q8MJ20; (TrEMBLrel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
FAB receptor (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 30.8 tes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
 1173
1174
1107
1107
1100
1100
1130
1130
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SMART; SM00208; TNFR; 3.

PROSITE; PS01186; EGF 2; UNKNOWN 1.

PROSITE; PS00652; TNFR NGFR 1; 1.

NON TER 146 146

SEQÜENCE 146 AA; 164487 MW; 1C91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8SQ52;
01-JUN-2002 (
01-JUN-2002 (
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 GOFCRNPCPPGERKARDCTVNEDEPDCVPCQEGKEYTDKGHFSSKCRRCRLCDEGHGLEV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22760275; PubMed=12878204; DOI=10.1016/S0006-291X(03)01304-4; Bridgham J.T., Johnson A.L.; "Characterization of chicken TNFR superfamily decoy receptors, DcR3 and osteoprortegerin."; Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Brothys. Res. Commun. 307:956-961(2003). EMBL; AY251407; AAP03890.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                   Euteleostomi;
                                                                                                                                                                                                              SEQUENCE FROM N.A. Petit F., Arnoult D., Lellevre J.-D., Lecossier D., Hance A.J., Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 15.6%; Score 161.5; DB 2; Length 130; 1 Similarity 31.7%; Pred. No. 3.3e-06; 32; Conservative 12; Mismatches 50; Indels 7
                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                         Estaquier J.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF530075; AAM95635.1; -.
HSSP; 014763; 1DU3.
                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006915; P:immune response; IEA.
GO; GO:0007165; P:immune response; IEA.
InterPro; IPRO08063; Fas receptor.
InterPro; IPRO01368; INFR.C6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 LENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Fas receptor CD9 (Fragment).
Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00020; TNFR_c6; 2.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR006509; EGF like.
InterPro; IPR001368; TNFR_GG.
Pfam; PF00020; TNFR_G6; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                      NCBI_TaxID=9544;
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NON TER
NON TER
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    VARAN KARAN 
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                                                                                                                                                                                                                                                                                                                                                 83 CSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDC--- 138
                                                                                                                                                                                                                                                                                                                                                                                                                      -------KHTECPPGF 128
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                                                                                                                                                                                                           24 CRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQA-CDEQASQVALEN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 DCGALHRHTRLLCSRRDTDCGTCLPGFYEHG--DGCVSCPTSTLGSCPERCAAVCGW 173
                                                                                                                                                                                                                                                   41 CNQCPPGSYVKQHCT-AASPTVCAPCP-DQYYAEDWNSNDECQYCSAVCKE--LQYIKQE
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Best Local Similarity 28.3%; Pred. No. 6.6e-05;
Matches 39; Conservative 13; Mismatches 49; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
"Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fas (Fragment).
Belis silvestris catus (Cat).
Eukaryota, Metazca; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0000165; P:immune response; IEA.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; INFR_c6.
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147 AA; 16751 MW; 0E192AC4DCE1001F CRC64;
146 AA; 16487 MW; 1C9E64FE3A0FC2DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00020; TNFR_c6; 2.
PRINTS; PR01680; FASRECEPTOR.
SMORT; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR, NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Immunogenet. 31:159-166(2004).
EMBL; AB072009; BAB86798.1; -.
HSSP; 014763; ID4V.
                                                                                                                                                                                                                                                                                                                                                                                                                   97 CTSTODRVČEČIEGWYLELEF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 GTCLPGFYEHGDGCVSCP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 GVAQPGTPESDTVČFCČP 146
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Krzesz R., Hecker M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Q8SQ49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 SHPSPRCRRCKICDEEHGLEVEKNCTRTQNTKCRCKSNFF--CNVSQC-----DHCNPCM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Wistar; TISSUE=Smooth muscle; MEDINE-99330195; Pubmed=10403401; DOI=10.1016/S0014-5793(99)00683-3; Krzesz R., Wagner A.H., Cattaruzza M., Hecker M.; "Cytokine-inducible CD40 gene expression in vascular smooth muscle cells is mediated by nuclear factor kappaB and signal transducer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
"Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
                                                                                                                                                                                                                                                                              Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.9%; Score 133.5; DB 2; Length 124; 29.4%; Pred. No. 0.00072; ive 12; Mismatches 23; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 DCGALHRHTRLLCSRRDTDCGTCLPGFYEHG--DGCVSCPTS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO, GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:00006915; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; TNFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 AA; 14319 MW; 15A7DFF058D79942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 AA
                                                                           124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bur. J. Immunogenet. 31:159-166(2004).
EMBL; AB072010; BAB86799.1; -.
HSSP; 014763; 1D0G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUE=Smooth muscle;
                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activator of transcription-1.";
FEBS Lett. 453:191-196(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001368; TNFR_C6.
Pfam; PF00020; TNFR_C6; 2.
PRINTS; PR01680; FASRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD40 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                    Fas delta6 (Fragment).
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Local S...
30;
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NON TER
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                                                                       088051
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09JKE0
109JKE0
AC 09JKE0
DT 01-0
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   RESULT 5
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66 ARCQACD-EQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLD---CG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 HQHRHCELNQGLQVKKEG-TAVSDTVCTCKEG-----QHCASKE---CETCAQHRPCG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 RCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSE--C 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 OCVICSDKQYLQGGECCDLCQPGNRLVSHCT-ALEKTQCQPCDSGEFSA---HWNREIRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
"Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
15a delta 5 delta 6 (Frament).
Felis silvestris catus (Gat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 12.3%; Score 127.5; DB 2; Length 169; I Similarity 29.7%; Pred. No. 0.003; 44; Conservative 14; Mismatches 69; Indels 21.
                                                                                                                                                                                                                                          HOST; W242920; LUNA.

GO; GO:0016620; C:membrane; IEA.

GO; GO:0004888; F:transmembrane receptor activity; IEA.

GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0006955; P:immune response; IEA.

GO; GO:0001655; P:signal transduction; IEA.

InterPro; IPR008063; Fas_receptor.

InterPro; IPR001865; Ribosomal_S2.

InterPro; IPR001368; TNFR_c6.

Pfam; PF00020; TNRR c6; 1.

PRINTS; PR01680; FASRECEPTOR.

SMART; SM0208; TNFR.; 3...

SMART; SM0208; TNFR.; 3...
SEQUENCE FROM N.A., STRAIN-WHOLE; STRAIN-WHOLEZ; TISSUE-Smooth muscle; Gao D., Hecker M.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Immunogenet. 31:159-166(2004).

EMBL; AB072012; BAB86801.1; -.

EMBL; AB072012; Chembrane; IEA.

GO; GO:0006918; Fitransmembrane receptor activity; IEA.

GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0006955; P:immune response; IEA.

GO; GO:0007165; P:sigmal transduction; IEA.

InterPro; IPR008063; Fas receptor.

InterPro; IPR001368; TNFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 AA; 18525 MW; F199D91EFA224A26 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 ALHRHTRLLCSRRDTDCGTCLPGFYEHG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :: || | | | :: |
127 PGFGVVQMATETTDTVCQPCPVGFFSNG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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SMART; SM00208; TNFR; 1.
                                                                                                                                                                          EMBL; AF241231; AAF43717.2;
HSSP; Q92956; LJMA.
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Best Local Similarity
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34; Conservative
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                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
                                                                                                                                                                                                              Query Match
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Q6VZR1;
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Matches
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Q8BDC5
ID Q8BDC
                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                               59 NHHNSECARCOACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 CQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHT 127
                                                                                                                                                                                      10 SHFSPRCRRCKICDEEHGLEVEKNCTRIQNIKCRCKSNPF--CNVSQC-----DHCNPCM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 RCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECAR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 KCICSSNYYSQLSSLVCRAC----ISPCLECLDDA--LALPAD------GTQCVT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 CQP-----GLNRIIDNVNNKCNCLDGYYETTGVLACTQCSP----PCYDC-----
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name-fur;
Paramecium aurelia.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                    7;
                                                                  Query Match 12.2%; Score 126.5; DB 2; Length 65; Best Local Similarity 36.7%; Pred. No. 0.0016; Matches 22; Conservative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.0%; Score 125; DB 2; Length 110; 22.4%; Pred. No. 0.0034; ative 17; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=2998-axenic;
Wyroba E., Wiejak J., Surmacz L.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=2998-axenic;
Wyroba E., Wiejak J., Surmacz L.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF351195; AAK27160.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 1
65 AA; 7670 MW; A557395A3D527417 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BIR3;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 RLLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ADNGT-----GAECTTCPPGTFTLC 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR006209; EGF like.
Interpro; IPR009030; Grow fac recept.
PROSITE; PS01186; EGF 2; ÜNKNÖWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Conservative
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paramecium.
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=fur;
                                                                                                                                                                                                                                                                                                                                                 O9BIR2;
                                                                                                                                                                                                                                                                                                                         Q9BIR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9BIR3
                                                                                                                                                                                                                                                                            RESULT 8
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68 CQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 RCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECAR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 AGDFHKKI-GLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 ASTYRSKINSSLICDMCPPGYYKNKDCTS-TSTTICLPCGEGEYTAY-NNSLTKCIRCKD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 COP-----GIARIIDNINNKCNCODGYYETTGVLACTQCSP----PCYDC-----
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC VR-111;
PubMed=14671117; DOI=10.1128/JVI.78.1.353-366.2004;
PubMed=14671117; DOI=10.1128/JVI.78.1.353-366.2004;
Fulman E.R., Afconso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
J. Virol. 78:353-366(2004).
J. Viro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.9%; Score 124; DB 2; Length 110; 21.8%; Pred. No. 0.0041; tive 19; Mismatches 51; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.9%; Score 124; DB 2; Length 117; 27.8%; Pred. No. 0.0043; ive 20; Mismatches 46; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 RLLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ADNGT-----GAECTTCPPGTFTLC 108
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EMBL; AF351194; AAK27159.1; -.
HSSP; P12940; 1C2A.
InterPro; IPR006209; EGF like.
InterPro; IPR009030; Grow_fac_recept.
PR051TE; P801186; EGF 2; ÜNKNÖWN_1.
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Created)
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                       :: ||:: :| | |
82 ITVRNCTSTNNTVCASK 98
           78 VALENCSAVADTRCGCK 94
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                                                                                  PRELIMINARY;
                                                                                                      05-JUL-2004 (TrEMBLrel.
                                                                                                                (TrEMBLrel.
                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                  Q6P2H9
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                                                             RESULT 13
                                                                       Q6P2H9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 KIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQ 77
                                                                                                                                                     18 GGSKM----CKPD-EVKLGNQCCPPCGSGQKVTKVCTENSG-ITCTLCPNGTYLT--GLY
                                                                                                                                                                                                                                                                                                                                     2 GGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPODTFLAWENHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Gaps
                                                                                                                                             "Polymorphisms of the cytomegalovirus (CMV) -encoded tumor necrosis
                                                                                                            MEDLINE=22242165; PubMed=12355354;
Arav-Boger R., Willoughby R.E., Pass R.F., Zong J.C., Jang W.J.,
Alcendor D., Hayward G.S.;
                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.7%; Score 121.5; DB 2; Length 172; 33.8%; Pred. No. 0.0098; ive 14; Mismatches 30; Indels 7;
                                                                                                                                                                                                                                                                                            11.8%; Score 123; DB 2; Length 167; 32.3%; Pred. No. 0.0072; tive 16; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              He R., Ruan Q.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF1322031; AAK60563.1; -.
HSSB; Q92956; 1JMA.
                                                                                                                                                                                                                                                                       167 AA; 18339 MW; C2495E13230E9616 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                   Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
       01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                              62 NSECARCQACDEQASQVALENCSAVADTRCGCK 94
                                                                                                                                                                                                                                                                                                                                                                                        70 N--CTNCTQCND--TQITVRNCTSTNNTICASK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0004812; F:receptor activity; IEA. Pfam; PF00020; TNFR G6; 1. SMART; SMO0208; TNFR, C6; 1. PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1. PROSITE; PS50050; TNFR NGFR 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                      Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26; Conservative
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cytomegalovirus
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      Local Similarity
nes 30; Conserv
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                                        UL144 (Fragment)
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SEQUENCE
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Matches
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley D.M., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 CCSLCQPGQKLVSDCTE-FTETECLPCGESEFLDTWNRETHFHQH----KYCDPNLGLRV 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 CCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFL-AW--ENHHNSECARCQACDEQASQVA
                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IISSUE=Pancreas;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.5%; Score 119; DB 2; Length 151; 27.8%; Pred. No. 0.014; tive 13; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; 1.
EBAA27CE7592172B CRC64;
                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
151 AA.
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PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 3.
PROSITE; PS00186; EGF 2; UNKNOWN 1.
PROSITE; PS00652; TNFR NGFR 1; 1.
PROSITE; PS50050; TNFR NGFR 1; 1.
SEQUENCE 151 AA; 17079 WW; EBAA27
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Lewis S.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 QLGNQCCPPCKQGYRVTGQCTQ-YTSTTCTLCPNGTYVS--GLYN--CTNCTECND--TE 81
                                                                                                                                                                                                                                         MEDLINE=22242165; PubMed=12355354;
Arav-Boger R., Willoughby R.E., Pass R.F., Zong J.C., Jang W.J.,
Alcendor D., Hayward G.S.;
Alcendor D., Hayward G.S.;
Polymorphisms of the cytomegalovirus (CMV)-encoded tumor necrosis
factor-alpha and beta-chemokine receptors in congenital CMV disease.";
J. Infect. Dis. 186:1057-1064 (2002).
EMBL; AF498087; AAN37946.1; -.
HSSP; Q92956; JUMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22667250; PubMed=12782278; DOI=10.1016/S0925-4773(03)00019-4; Rascle A., Stowers R.S., Garza D., Lepesant J.-A., Hogness D.S.; "L63, the Drosophila PFTAIRE, interacts with two novel proteins unrelated to cyclins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TYEMBLEEL. 20, Created)
01-MAR-2002 (TYEMBLEEL. 20, Last sequence update)
25-OCT-2004 (TYEMBLEEL. 28, Last amontation update)
25-OCT-2004 (TYEMBLEEL. 28, Last amontation update)
PFTALRE-interacting factor 2 (CG31483-PA).
Name-Pif2; Synonyms-PIF-2; ORFNames-CG31483;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Badopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                              10.7%; Score 111.5; DB 2; Length 166; 28.6%; Pred. No. 0.066; ive 20; Mismatches 28; Indels 7
166 AA; 18411 MW; 193D55AE19E046FA CRC64;
                                                                                                                                                                           Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                            166 AA.
                                                                                                                                                                                                                                                                                                                              GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR001368; TWFR c6.
Pfam; PF00020; TWFR c6; 1.
SMART; SM00208; TWFR, 1.
                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                             PRT;
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No SEQUENCE FROW N.A.

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REDILINES_2015 GORD PARCES_1073112; DOI=10.1126/science_207.5461.2185;
Addams N.D. Cealaker S.E., Hölt R.A., Davine C.A., Gocarge J.D., Addams N.D., Cealaker S.E., Scheers S.E., 16 PM. W. Dokines N.A., Galle R.F., Addams N.D., Cealaker S.E., Scheers S.E., 16 PM. P. D., Zangol Q., Chen L.X., D. M. Cearge M. C.A., Levis S.E., N. Holl R.A., Mannatides P.C., Daving M.C., Estificate D.D., Annual M.C., Changer S.E., Scheers J.E., Change M.C., Estificate D.D., Annual M.C., Changer S.E., Scheers J.E., Change M.C., Estificate D.D., M. Chill J.Y., Pages J.M., Ball M. H.J., Mackers, Fichacker D. Elandwin D., M. Chill J.Y., Pages J.M., Ball M. H.J., Mackers, Fichacker D., Bolchan M., Ball M. M., Bouck J., Bucketcin P., Brandshow S., Borkwow D., Bolchan M.R., Bouck J., Bucketcin P., Brandshow S., Borkwow D., Bolchan M.R., Bouck J., Brandshow J. B. Brandshow S., M. Changer S., Changer M., Chander J., Bayershow D., Bolchan M., Bouck J., Brandshow J. Brandshow D., Bolchan M.R., Bouck J., Brandshow J. Brandshow D., Bolchan M.K., Bouck J., Brandshow J. Brandshow D., Bolchan M.K., Bouck J., Brandshow J. Brandshow D., Bolchan M.K., Bouck J., Brandshow J. Brandshow D., Brandshow D., Bolchan M.K., Maller M., Gulde W. C., Goner J., Changer J., Mackel J., Maller M., Gulde W., Gong F., Gorrell J.H., Gul Z., Gulan P., Marris M., Gulde W., Marris M., Gulde W., Marris M., Mallerina M.V., Mobarry C., Morris J., Monker M., Gulde W., Mallerina M.Y., Molden M. T., Mell M.H., Indeyson C., Mallerina M.Y., Molden M. A., Maller M., Maller M., Maller M.Y., Molden M.Y., Molden M., Maller M., Mall
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Query Match 10.5%; Score 109; DB 2; Length 118; Best Local Similarity 23.8%; Pred. No. 0.08; Matches 41; Conservative 3; Mismatches 62; Indels 66; Gaps 10;
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                                                                   FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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FlyBase SEQUENCE (WAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AF273708; AAL35411.1; -.
EMBL; AF203674; AAF54113.3; -.
HSSP; P21860; 1M6B.
FlyBase; F8901046673; Pif2.
PROSITE; PS01208; VWFC_1; UNKNOWN 1.
SEQUENCE 118 AA; 11566 MM; AFGFDISA61FF5C81 CRC64;
systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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Search completed: June 27, 2005, 14:22:24 Job time : 175 secs

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Brondyk W, Jiang X,
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GenCore version
Copyright (c) 1993 - 2005
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Listing first 45 summaries
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                              protein search, using sw model
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Adl17744 Adj56817 Aar24083 Aar78612	Aab36228 Aab37675 Adm46624 Ada49701	Aaw50286 Aaw50288 Ada49708 Aab36229 Aar24084	Abw02714 Adj45750 Aar24081 Aaw52268	Adf57549 Aaw52276 Aaw89238
ADL17744 ADJ56817 AAR24083 AAR78612	AAB36228 AAB37675 ADM46624 ADA49701	AAW50286 AAW49708 AAB36229 AAR24084	ABW02714 ADJ45750 AAR24081 AAW52268	ADF57549 AAW52276 AAW89238
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17.5 17.5 16.4	15.9 15.9 15.8	15.7 15.7 15.7 15.7		14.1 14.2 1.2.2
181.5 181.5 170.5	165.5 165.5 164.5 162.5	162.5 162.5 162.5 162.5 161	155.5 155.5 152.5 149.5	147.5 147 147
28 28 28 28	33 33 33	33 33 34 34 34 34 34	0 4 4 4 0 1 2	4 4 4 5 4 5

ALIGNMENTS

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expression level in yeast than did a wild-type INFrED clone. The encoded polypeptide contained these 2 amino acid substitutions. The introduction of proline residues may assist the polypeptide to adopt a favourable conformation that fixes the neighbouring cysteine residue into the correct orientation for disulfide bond formation, resulting in a higher yield of correctly folded proteins in yeast or mammalian host cells. The invention therefore provides methods of increasing protein expression levels by substituting an amino acid residue with proline, where the substitution occurs within 15 (preferably within 10, and especially within 5) amino acids of a cysteine residue. Note: The present sequence is not shown in the specification but is derived from the TNFrED sequence given in figure 4 (see ABR62363)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPQNNSICCTKCPKGTYLYNDCPGPGQDTDCRECEIGSFTASENHLR-HCLSCSKCRKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease; immunodeficiency; metastasis; haemolytic ansemia; asthma; X-linked SCID; severely combined immunodeficiency; apoptosis inhibition; Alzheimer's disease; Parkinson's disease; Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecule encoding a human tumor necrosis factor receptor 2 and its two splice variants, useful for treating arthritis or inflammation, cancer (such as follicular lymphomas) and immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      necrosis factor-receptor related protein; TR2; human; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.9%; Score 206.5; DB 6;
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ROSEN C A.
GENTZ R L.
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This invention relates to an isolated nucleic acid molecule encoding a human tumour necrosis factor(TNF)-receptor related protein TR2. Included in the hirvention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.

The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a member of the TNFR superfamily. The invention includes a method for the treatment of arthritis or inflammation using an antibody directed against a fragment of the TR2 protein. TR2 its agonists and antibody directed against cartisousuppressive, antialeragic, antiathritic, antiashmatic, antiathratic, antiathra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as sources for generating antibodies, as molecular weight markers. This sequence represents the tumour necrosis factor receptor (TNFR) domain of the human TNFR-1 protein. The sequence was used in the characterisation of the TR2 receptor protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.3%; Score 200.5; DB 3; Length 154; 29.8%; Pred. No. 1.7e-07; Live 20; Mismatches 72; Indels 21;
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                      Disclosure, Fig 16, 373pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA49698 standard; protein; 154 AA
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960S-0030157P. 970S-00822953. 980S-0003886. 980S-00027287. 990S-00552656.

20-FEB-1998; 19-FEB-1999; 07-JAN-1998 20-FEB-1998

21-MAR-1997

11-MAR-1999 04-JUN-1999 06-JUL-1999

10-MAR-2000; 2000US-00523323.

99US-0137457P. 99US-0142657P. 99US-0148326P. 99US-0168380P.

GENOME SCI INC

(HUMA-) HUMAN 02-DEC-1999;

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The present invention relates to the isolation of a biologically active Apo-2 ligand inhibitor (Apo-2LI) or Apo-3, and the polynucleotide sequences encoding them. Apo-2LI and Apo-3 are involved in apoptosis. The Apo-2LI and Apo-3 polypeptides are useful in diagnostic assays. Apo-2LI is useful for generating antibodies, as standards in assays for Apo-2LI Apo-2LI, in affinity purification techniques, and in competitive-type receptor binding assays when labelled with radioiodine, enzymes or inducing apoptosis in cancer cells, and thus have therapeutic utility. The present sequence represents the extracellular region of a human TNF receptor family protein. This sequence is compared with the extracellular region of human Apo-2LI.
                                                                                                                                                                                                                          Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or Apo-3 polypeptide which induces or stimulates apoptotic activity, useful in diagnostic assays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; apoptosis inducing molecule II; AIM II; antibody; tumour necrosis ligand superfamily; lymphotoxin-bera receptor; TR6; TRAIL receptor 6; lymphadenopathy; aberrant bone development; autoimmune disease; graft-versus-host disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.3%; Score 200.5; DB 6; Length 154; 29.8%; Pred. No. 1.7e-07; tive 20; Mismatches 72; Indels 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human tumour necrosis factor receptor-I cysteine rich motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL17741 standard; protein; 154 AA
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                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 53pp; English.
                                                96US-00625328.
96US-00710802.
97US-00828683.
              28-MAR-2002; 2002US-00112793.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 154 AA;
                                                                                                                                                         Ashkenazi AJ;
                                                     01-APR-1996;
                                                                    23-SEP-1996;
31-MAR-1997;
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protein comprising a protein whose sequence comprises an immunogenic fragment of the amino acid residues 68-240 of the Human apoptosis inducing molecule II, AIM II, appearing as ADL17690 or a protein whose sequence comprises at least 30 or 50 amino acid residues 68-240, where the fragment comprises at least 30 or 50 amino acid residues 68-240, where the fragment comprises at least 30 or 50 amino acid residues. Also included are a hybridome that produces the antibody, a method of detecting in a biological sample a protein that binds the antibody or its portion, a composition comprising the antibody and a carrier and an isolated cell that produces the antibody. Human AIM II is a member of the tumour necrosis ligand superfamily and has been shown to bind lymphotoxin-beta receptor and TR6 (TRAIL receptor 6). The antibody is useful for preparing a composition for treating e.g., lymphadenopathy, aberrant bone development, autoimmune disease, graft-versus-host disease, rheumatoid arthritis, osteoarthritis or cancer (many other diseases and conditions are listed in the specification). The present sequence represents a cysteine-rich motif from a protein thought to bind AIM II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein, useful for preparing a composition for treating e.g., lymphadenopathy, autoimmune disease, rheumatoid arthritis, osteoarthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated antibody or its portion binding to a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibody that binds to human Apoptosis Inducing Molecule II (AIM II)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.3%; Score 200.5; DB 7; Length 154; 29.8%; Pred. No. 1.7e-07; Indels 21.
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                                                                                                                                                                                                                                                                                                                                                                                Ebner R, Yu G, Ruben SM, Ullrich S, Zhai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 13; SEQ ID NO 53; 163pp; English
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Best Local Similarity
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133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-1989;
                                                                                                                                                                                                          14-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to apoptosis inducing molecule II (AIM III), a TNF (tumour necrosis factor)-ligand superfamily member and its corresponding nucleic acid sequence. The invention is useful for preventing, treating, ameliorating, diagnosing or prognosing graft versus host disease, immunodeficiency, cancer, autoimmune diseases such as multiple sclerosis, type I diabetes, rheumatoid arthritis, primary biliary cirrhosis, aplastic ansemia, myelodysplasia, systemic lupus erythematosus and idiopathic thrombocytopenic purpura. It is useful for screening or identifying compounds capable of enhancing or inhibiting cellular response induced by AIM II, for inhibiting, blocking or reducing T-cell activation. AIM II is useful as a molecular weight marker on SDS-PAGE gels or on gel filtration columns. The present sequence is a cysteinerich motif of human TNF receptor (TNFR) family member.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated apoptosis inducing molecule II polypeptide, useful for treating, preventing, ameliorating, diagnosing or prognosing autoimmune diseases such as multiple sclerosis, rheumatoid arthritis, aplastic anemia.
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                                 Apoptosis inducing molecule II; AIM II; TNF; tumour necrosis factor; therapy; graft versus host disease; immunodeficiency; cancer; autoimmune disease; multiple sclerosis; type I diabetes; rheumatoid arthritis; primary bilary cirrhosis; aplastic anaemia; myelodysplasia; systemic lupus erythematosus; didiopathic thrombocytopenic purpura; cellular response; T-cell activation; molecular weight marker; human; TNF receptor; TNFR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ullrich S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 13; SEQ ID NO 53; 189pp; English
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Human TNFR-I cysteine-rich motif.
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96US-0030157P.
97US-0082253.
98US-00027287.
98US-0027287.
99US-0124041P.
99US-0124041P.
99US-0143427P.
99US-0148326P.
99US-0148326P.
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76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel polynucleotide sequences encoding tumour necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP). The products of the invention are useful in pharmaceutical compositions for prophylaxis or treatment of human tumours and to understand the mechanisms of TNF action. This sequence represents a fragment of the TNF-BP described in the disclosure of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                         TNF; human; tumour necrosis factor; tumour necrosis factor receptor; TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.
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118 EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
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                                                                                                                                                                                                                                                                                                                                                            Human TNF binding protein fragment.
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                                                                                                                                                                         ABG74752 standard; protein; 161
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89DE-03920282
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GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC-----FNCSLCLN-GTVH----LSCQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment of acute or chronic inflammatory disease, e.g. leukaemia - by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate.
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                                                                                                     Human, tumour necrosis factor; TNF; TNF receptor type I; inflammatory disease; leukaemia; TNF binding protein; anti-inflammatory drug; methotrexatess.
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                                       Human soluble tumour necrosis factor receptor type I.
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97US-0036355P.
97US-0039315P.
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23-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New ethylene! glycolated polypeptide(s) with improved pharmacokinetic properties - for treating e.g. TNF and IL-1 mediated diseases, e.g. adult respiratory distress syndrome, rheumatoid arthritis, septic shock etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence shows a native 30 kD TNF inhibitor which may be modified to contain at least one non-native cysteine residue, pref. at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is joined to a non-peptidic polymer, pref. monomethoxy PEG via thio-ether bonds. Two such TNF inhibitor mols may be linked via this non-peptidic spacer. The modified polypeptides show improved pharmokinetic properties, i.e. increased mol. w. hence reduced clearance rate following s.c. or systemic administration, increased sol. of native TNF inhibitors, and reduced antigenicity. The polypeptides may be used for treatment of TNF mediated diseases such as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid arthritis, inflammatory bowel disease and septic shock. The same method may be applied to the interleukin-1 receptor antigonist IL-1ra. See also AAR27495. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                  Tumour necrosis factor; ethylene glycol; pharmokinetic; adult respiratory distress syndrome; rheumatoid arthritis; septic shock; pulmonary fibrosis; spacer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 54; Fig 2; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW59664 standard; protein; 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-US002122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91US-00669862.
92US-00822296.
                                    (first entry)
                                                                                                 Native 30 kD TNF inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Armes LG,
   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYND ) SYNERGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-348933/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 48; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thompson RC,
                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                            WO9216221-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-1992;
25-MAR-2003
09-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1992
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7;

Gaps

21;

69

AAW59664;

SXXXE

RESULT 8 AAW59664

Query Match

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chimeric; fusion; dimerisation domain; autoimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
             inflammation, apoptosis.
                                                                                                                                                                                         3oyle WJ, Wooden S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                 WPI; 1999-034661/03
                                                                                                                                                                (AMGE-) AMGEN INC.
                                                                                                                                                                                                                              N-PSDB; AAV81732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 161 AA;
                                                                                                                                        01-MAY-1997;
                                       Homo sapiens
                                                              409849305-A1
                                                                                                                29-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB37676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
AAB37676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the human soluble tumour necrosis factor receptor (sTNFR). The protein was used to make the truncated sTNFR proteins of the invention. The truncated sTNFR proteins and tumour necrosis factor binding proteins (TNBP) are used to treat any TNF-mediated disease, e.g. arthritis, adult respiratory distress syndrome, cachexia/anorexia, cancer, chronic fatigue syndrome, graft rejection, Alrahemer's diseases and other autoimmune diseases. Cells transformed with a vector containing DNA encoding the protein may be used for production of recombinant sTNFR, which may also be used for measuring the amount of sTNFR; in samples and to raise antibodies against sTNFR. TNPR may also be used in preparation of therapeutic compositions for treating the above diseases. The sTNFR deamidation site in region 111-126, so are more stable in vivo); contain fewer disulphide bonds and fewer epitopes, making them less antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fruncated and soluble forms of tumour necrosis factor receptor - useful for treating diseases involving factor, e.g. arthritis and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 EKQNTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 19.3%; Score 200.5; DB 2; Best Local Similarity 29.8%; Pred. No. 1.8e-07; Matches 48; Conservative 20; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour necrosis inhibitor 30 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW89233 standard; protein; 161 AA
                                                                                                                                                                                                     Kieft GL;
                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1; 205pp; English
                                                                                                             96US-0032534P.
97US-0037737P.
97US-0039314P.
97US-0039792P.
                                                                                                                                                                                                                                                                            for treating diseases involvir
respiratory distress syndrome.
                                                                         97WO-US012244
                                                                                                  96US-0021443P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     than full-length proteins
                                                                                                                                                                                                    Edwards CK,
                                                                                                                                                                                                                             WPI; 1998-101052/09
                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                          N-PSDB; AAV19801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 161 AA;
                        WO9801555-A2
 Homo sapiens
                                                                         09-JUL-1997;
                                                                                                                                                   04-MAR-1997;
                                                 15-JAN-1998
                                                                                                  09-JUL-1996
                                                                                                                           23-JAN-1997,
07-FEB-1997,
                                                                                                                                                                                                    Fisher EF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW89233
                                                                                                                06-DEC
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ID AAW8
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AC AAW8
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DT 04-M
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The present invention describes a chimeric polypeptide (A1), comprising am nosteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (I) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders tumour necrosis factor (TMF) /OPG and TMF receptor (TMF)/OPG chimeras are used to treat any INF receptor (TMF)/OPG chimeras are used to treat TMF and TMF-mediated disorders such as inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents the TNF inhibitor 30 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 GOVEISSCTVDRDIVCGCRRNOYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 SQVALENCSAVADTRCGCKPGWFVEC --- QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR-mediated disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin; IL-1; inflammatory disease; degenerative disease; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.3%; Score 200.5; DB 2 29.8%; Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB37676 standard; protein; 161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig 2, 92pp, English.
98WO-US008631.
                                                                                           97US-00850188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human 30 kDa TNF inhibitor.
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The present sequence is the protein sequence of the extracellular domain of the p55 tumour necrosis factor receptor (TNFrED). Screening of TNFrED mutant clones using a yeast display system yielded 2 mutant clones (see ABR62364 and ABR62365) that showed higher expression levels in yeast than in wild-type TNFrED. The first clone contained a proline residue that substituted the native Ser-87 residue (position 76 of the present sequence). The other clone contain a proline residue that substituted the native list-37 residue (23 of the present sequence) and also an isoleucine residue that substituted the native Ils-57 residue (46 of the present sequence) of TNFrED. The invention provides methods of increasing protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression levels by substituting an amino acid residue with proline, where the substitution occurs within 15 (preferably within 10, and especially within 5) amino acids of a cysteine residue. The introduction of proline residues may assist the polypetide to adopt a favourable conformation that fixes the neighbouring cysteine residue into the correct orientation for disulfide bond formation, resulting in a higher yield of correctly folded proteins in yeast or mammalian host cells
                                                                                                                                                                                                                                                                                                                                                                                            Increasing expression of a protein, comprises substituting at least one codon in the polynucleotide encoding the protein, for a codon encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 SQVALENCSAVADTRCGCKPGWFVEC -- QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; tumour necrosis factor inhibitor; 30kDa TNF inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
/note= "corresponds to wild-type Ser57
                                    "corresponds to wild-type Ser87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 RRDIDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.3%; Score 200.5; DB 6; 29.8%; Pred. No. 1.8e-07; ive 20; Mismatches 72;
                                                                                                                                                                                                                                                   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
                                                                                                                                                                                                                                                                                          Schweickhardt RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA20577 standard; protein; 161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 30kDa TNF inhibitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 4; 53pp; English
                                                                                                                                                                                                            30-NOV-2001; 2001US-0340648P.
                                                                                                                                                                  21-NOV-2002; 2002WO-EP013059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 29.8 Matches 48; Conservative
                                           /note=
                                                                                                                                                                                                                                                                                          Brondyk W, Jiang X,
                                                                                                                                                                                                                                                                                                                                   WPI; 2003-523245/49
                   Misc-difference 76
                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ACC84134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 161 AA;
                                                                                  WO2003046160-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-2003
                                                                                                                         35-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         proline.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to Tumour Necrosis Factor (TNF) inhibitors (see AAB37676 and AAB37685), which have TNF inhibitory activity. The novel TNF inhibitors of the present invention are useful as therapeutic agents for inhibiting the activity of TNF and interleukin (IL-1), and for treating inflammatory and degenerative diseases mediated by TNF. The 30 kba TNF inhibitor can inhibit TNF alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-native cysteine residue cross-linked with polyethylene glycol, useful for treating inflammatory and degenerative diseases mediated by TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "corresponds to wild-type His34 residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor; receptor; proline; protein engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.3%; Score 200.5; DB 4; Length 161; 29.8%; Pred. No. 1.8e-07; ive 20; Mismatches 72; Indels 21;
                                                                                                                                                                                                                                                                                                                                                         Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour necrosis factor receptor extracellular domain
                                                                                                                                                                                                                                                                                                                                                       King MW, Hale KK, Brewer MT, RW, Vannice J, Kohno T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR62363 standard; protein; 161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 19; 82pp; English
                                                                                                                                                                                                       89US-00450329.
90US-00479661.
90US-00555274.
                                                                                                                                             95US-00375242
                                                                                                                                                                                      39US-00381080
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                                                                                                                                                                                                                                                                                                                                                                                                                      2001-006443/01.
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                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAC83945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 161 AA;
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                                                                                                                                                                                                                                                                                                                                                                               Vanderslice RW,
                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                               19-JAN-1995;
                                                                                                                                                                                                                                                                      09-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
                                                            US6143866-A.
                                                                                                                                                                                                          11-DEC-1989;
07-FEB-1990;
                                                                                                                                                                                      18-JUL-1989
                                                                                                   07-NOV-2000
                                                                                                                                                                                                                                                     19-JUL-1990
                                                                                                                                                                                                                                                                                                                                                           Squires C,
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07-JUN-1995;
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                                                                                    19-JAN-1995;
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                                                      18-JUL-1989
                                                               11-DEC-1989;
07-FEB-1990;
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             01-APR-2003
                                                                                                                              Brewer MT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of novel human tumour necrosis factor (TNF) inhibitor polypeptides (designated 30kDa TNF inhibitor), and the polynucleotide sequences encoding them. Also disclosed is a fragment of the 30kDa TNF inhibitor polypeptide which comprises at least one non-native cysteine residue at the N-terminus, C-terminus, residue 14 or preferably 105. The polynucleotide sequence encoding the 30kDa TNF inhibitor manufacturing a medicament for treating a pathological condition mediated by TNF. The present sequence represents human 30kDa TNF inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQVALENCSAVADTRCGCKPGWFVEC -- QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                         New nucleic acid comprising a sequence that encodes a polypeptide having TNF inhibitory activity, useful for manufacturing a medicament for treating a pathological condition mediated by TNP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHIR-HCLSCSKCRKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, tumour necrosis factor inhibitor, 30kDa TNF inhibitor, 40kDa TNF inhibitor, TNF mediated pathological condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
40kDa TNF inhibitor; TNF mediated pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRDIDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 EKQNTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                19.3%; Score 200.5; DB 6; 29.8%; Pred. No. 1.8e-07; tive 20; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human 30kDa TNF inhibitor protein.
                                                                                                                                                                                                                                                                     Example 2; Fig 19; 85pp; English.
                                                                                                                                                                                  Kohno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA20579 standard; protein; 161
                                                                                                       89US-00381080.
89US-00450329.
90US-00479661.
95US-00375242.
                                                                                   95US-00484337.
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                                                                                                                                                                                 Thompson RC,
                                                                                                                                                                                                      WPI; 2003-531100/50.
                                                                                                                                                            (ANGE-) ANGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 161 AA;
                                                                                                       18-JUL-1989;
11-DEC-1989;
07-FEB-1990;
19-JAN-1995;
                      Homo sapiens
                                          JS6541620-B1
                                                                                  07-JUN-1995;
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                                                                                                                                                                                Brewer MT,
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 GÓVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human tumour necrosis factor receptor 1 (TNF-R1) protein, SEQ ID No 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interferon-beta; tumour necrosis factor receptor-1; erythropoietin;
thrombopoietin; inflammation; cancer; anaemia;
human tumour necrosis factor receptor 1; TNF-R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid comprising a sequence that encodes a polypeptide l
TNF inhibitory activity, useful for manufacturing a medicament for
treating a pathological condition mediated by TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.3%; Score 200.5; DB 6; Length 161; 29.8%; Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Mismatches
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                                                                                                                                                                                                                                                                                                                            Kohno T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 20; 85pp; English
                                                                   89US-00381080.
89US-00450329.
90US-00479661.
95US-00484337.
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N-PSDB; ADA20578.
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SQ Sequence 161 AA;
Query Match

Query Match

Best Local Similarity 29.8%; Pred. No. 1.8e-07;

Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps

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OY 16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 75

11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69

OY 76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLCS 132

DD 70 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119

OY 133 RRDTDCGTCLPGFYEHGDGCYSCPFSTLGSCPE--RCAAVC 171

Search completed: June 27, 2005, 14:18:38 Job time : 163 secs

120 EKONTVCŤĆHAGĚFLRENEČVŠĆ----SNČKKSLEČTKLĆ 155

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12 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASE-EHKRECLRCSRCRDKW
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Best Local Similarity 30.0
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RESULT 1
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Sequence 422, App
Sequence 13, Appl
Sequence 20, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Appl
Sequence 421, App
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Sequence 423, App
Sequence 430, App
                                                                                                                                                                June 27, 2005, 14:19:32 ; Search time 158 Seconds (without alignments) 423.490 Million cell updates/sec
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Sequence 19, 1
Sequence 21, 1
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1 QGGTRSPRCDCAGDFHKKIG......CPTSTLGSCPERCAAVCGWR 174
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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                       5.1.6
Compugen Ltd.
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1 US-10-218-102-422

US-09-798-789-13

US-09-798-789-20

4 US-10-218-102-423

4 US-10-218-102-423

US-10-218-102-431

US-10-218-102-421

US-09-798-789-11

US-09-798-789-11

US-09-798-789-11

US-09-798-789-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1717557 seqs, 384547976 residues
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                       GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                    - protein search, using sw model
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Match Length
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seq length: 174
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203.5
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201.5
201.5
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Maximum |
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Sequence 4, Appli
Sequence 4, Appli
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Sequence 2, Appli
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Sequence 1, Appli
Sequence 9, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
                Sequence 431, App
Sequence 3, Appli
Sequence 12, Appli
Sequence 12, Appl
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 53, Appli
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Sequence 17, Appl
Sequence 427, App
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Sequence 4, Appli
Sequence 10, Appl
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Patent No. US2002009780A1;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dahiyat, Bassil
APPLICANT: Discourage For The TREATHENT OF THE-ALPHA RELATED
TITLE OF INVENTION: UNBER: US/09/798, 789
CURRENT FILING DATE: 2001-03-02
PRIOR PRILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
SOFTWARE: PATENT UNCS: 22
SOFTWARE: PATENT UNCS: 22
SOFTWARE: PATENT UNCS: 22
SOFTWARE: PATENT UNCS: 22
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US-09-798-789-12
                                                                                                                           US-09-899-422-4
US-09-999-4224-4
US-09-899-4234-4
US-09-792-356-4
US-09-792-356-4
US-09-792-356-7
US-10-621-783-2
US-10-621-783-2
US-10-621-783-2
US-09-798-789-14
US-10-218-102-419
US-10-218-102-423
US-10-218-102-423
                          US-09-800-909-3
US-09-884-987-4
US-09-800-908-12
US-10-423-927-3
US-10-632-929-12
US-10-112-793-12
US-10-175-680-53
US-10-218-102-439
US-10-218-102-431
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US-09-405-032-126
US-10-467-243-4
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9

Gaps

73; Indels 19;

75

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; Sequence 423, Application US/10218102
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76 SQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDC--GALHRHTRLLCSR 133
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                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bentzien, Joerg
APPLICANT: Bentzien, Joerg
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Hayes, Robert J.
APPLICANT: Hayes, Robert J.
APPLICANT: Vielmetter, Jost
ITLE OF INVENTION: Protein Design Automation for Protein Libraries
FILE REFERENCE: A-6722-11/FFT/RNS/RMK
CURRENT APPLICATION NUMBER: US/10/218,102
FURNER TELING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/321,937
PRIOR APPLICATION NUMBER: US 60/351,937
PRIOR PILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/352,103
PRIOR PILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 432
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73; Indels 19; Gaps
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Patent No. US20020009780A1

GENERAL INFORMATION:
APPLICANT: Dahiyat, Bassil
APPLICANT: Filikov, Anton
TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: DISCOVERS
TITLE OF INVENTION: DISCOVERS
TITLE OF UNDENTION: DISCOVERS
THE TREATMENT APPLICATION NUMBER: US 60/186,427
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                                                                                                                           122 KONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 RDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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                                                                                                                                                                                                                                                                      Sequence 422, Application US/10218102
Publication No. US20030130827A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 48; Conserv
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LENGTH: 162
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APPLICANT: Filikov, Anton
TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: DISCROBERS
TITLE OF INVENTION: DISCROBERS
FILE REFERENCE: A-6990-1/RFT/RNS/RMK
CURRENT PELLICATION NUMBER: US/09/798, 789
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186, 427
PRIOR APPLICATION NUMBER: US 60/186, 427
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN OF 2.1
                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-798-789-13
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                                                                                                                                                                                                                                                                                                                                                              Query Match 19.8%; Score 205.5; DB 9; Length 162; Best Local Similarity 30.0%; Pred. No. 6.5e-09; Matches 48; Conservative 19; Mismatches 74; Indels 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 RDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/09798789; Patent No. US20020009780A1; GENERAL INFORMATION:
                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 162
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US-09-798-789-20
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LENGTH: 162
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Sequence 421, Application US/10218102
Publication No. US20030130827A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
  SOFTWARE: PatentIn version 3.1
                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                              ; OTHER INFORMATION: synthetic US-10-218-102-430
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US-10-218-102-421
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                               SEQ ID NO 430
LENGTH: 162
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           GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg
APPLICANT: Bentzien, Joerg
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dehiyat, Bassil I.
APPLICANT: Designatials, John R.
APPLICANT: Hayes, Robert J.
APPLICANT: Wielmetter, Jost
TITLE OF INVENTION: Protein Design Automation for Protein Libraries
FILE REFERENCE: A-6722-11/RF/RMS/RMY
CURRENT APPLICATION NUMBER: US/10/218,102
FRIOR FILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-09-10
PRIOR PLING DATE: 2001-09-25
PRIOR PLING DATE: 2002-09-25
PRIOR FILING DATE: 2002-01-25
PRIOR PLING DATE: 2002-01-25
SOFTWARE: Patentin version 3.1
SSOFTWARE: Patentin version 3.1
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APPLICANT: Bentzien, Joerg
APPLICANT: Bentzien, Joerg
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Hayes, Robert J.
APPLICANT: Hayes, Robert J.
APPLICANT: Vielmetter, Jost
ITLE OF INVENITON: Protein Design Automation for Protein Libraries
FILE REFERENCE: A-67229-11/RFF/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/218,102
CURRENT FILING DATE: 2002-08-10
PRIOR APPLICATION NUMBER: US 60/311,545
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/324,899
PRIOR PILING DATE: 2002-01-25
PRIOR PILING DATE: 2002-01-25
PRIOR PILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 432
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Publication No. US20030130827A1
GENERAL INFORMATION:
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Publication No. US20030130827A1

// OTHER INFORMATION: synthetic
US-10-218-102-423
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76 SQVALENCSAVADTRCGCKPGWFVECQ---VSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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; Patent No. US2002009780A1
; GRERAL INFORMATION:
; GRERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Dahiyat, Bassil
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: UNRIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: UNBERS: US/09/798, 789
; CURRENT FILING DATE: 2001-03-02
; PRIOR PILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARR: PATENTIN VET. 2.1
; SSOFTWARR: PATENTIN VET. 2.1
                                                                                                                                                                     12 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM
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US-09-798-789-11
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Query Match 19.8%; Score 205.5; DB 14; Length Best Local Similarity 30.4%; Pred. No. 6.5e-09; Matches 49; Conservative 20; Mismatches 71; Indels
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 173
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US-09-798-789-21
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                                                           APPLICANT: nayes, noces, of APPLICANT: vielmetter, Jost TITLE OF INVENTION: Protein Design Automation for Protein Libraries TITLE OF INVENTION: Protein Design Automation for Protein Libraries FILE REFERENCE: 4.67229-11/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US 03/927, 790
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-10
PRIOR PLILING DATE: 2001-09-10
PRIOR PLILING DATE: 2001-09-10
PRIOR PLILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-01-25
PRIOR PLING DATE: 2002-01-25
PRIOR PLING DATE: 2002-01-25
PRIOR PLING DATE: 2002-01-25
SPRIOR PLING DATE: 2002-01-25
SOFTWARE: Patentin version 3.1
SEQ ID NO 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.6%; Score 203.5; DB 14; Length 162; 30.0%; Pred. No. 9.3e-09;
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Patent No. US20020169118A1
GENERAL INFORMATION:
Bentzien, Joerg
Dahiyat, Bassil I.
Desjarlais, John R.
Hayes, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: synthetic
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Matches 48; Conservative
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60 HHNSECARCOACDEOASOVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQP 116
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                                                                                                                                                                                                                                                                        12 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 70
                                                                                                                                                                                                                                            3 GTRSPR---CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWEN 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 CLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                    Gape
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                                                               OTHER INFORMATION: Description of Artificial Sequence: recombinant; OTHER INFORMATION: TNR-BP sequence
US-09-899-429A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-798-789-19
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                                                                                                                                                        Length 173;
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                                                                                                                                                   Query Match
19.6%; Score 203; DB 9;
Best Local Similarity 29.4%; Pred. No. 1.1e-08;
Matches 52; Conservative 20; Mismatches 81;
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TYPE: PRT
ORGANISM: Artificial Seguence
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71 GQVEISSCTVDRDTVCGCRKNQYRHYKSENLFQC----FNCSLCLN-GTVH----LSCQ 120
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US-10-218-102-431
US-10-218-102-431
Sequence 431, Application US/10218102
Publication No. US20030130827A1
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg
APPLICANT: Bentzien, Joerg
APPLICANT: Hayes, Robert J.
APPLICANT: Wielmetter, Jost
TITLE OF INVENTION: Protein Design Automation for Protein Libraries
FILE REFERENCE: A-67229-11/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US 09/927, 790
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/352,103
PRIOR FILING DATE: 2002-01-25
PRIOR PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR PRIOR FILING DATE: 2002-01-25
PRIOR P
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                                                                                                              16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
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                                         Gaps
                                         21;
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19.4%; Score 201.5; DB 14; Length
Best Local Similarity 29.8%; Pred. No. 1.3e-08;
Matches 48; Conservative 20; Mismatches 72; Indels
Best Local Similarity 29.8%; Pred. No. 1.3e-08;
Matches 48; Conservative 21; Mismatches 71; Indels
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; Sequence 3, Application US/09800909
; Patent No. US20010019833A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                    APPLICANT: Dahiyat, Bassil
APPLICANT: Pilkov, Anton
TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: UARLIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: A-68990-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/798,789
CURRENT FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/186,427
PRIOR APPLICATION NUMBER: US 60/186,427
PRIOR FILING DATE: 2000-03-02
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NOS: 2.2
SOFTWARE: PALENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bentzien, Joerg
APPLICANT: Bentzien, John R.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Desjarlais, John R.
APPLICANT: Hayes, Robert J.
APPLICANT: Vielmetter, Jost
TITLE OF INVENTION: Protein Design Automation for Protein Libraries
FILE REFERENCE: A-67229-11/RFT/RMS/RMK
CURRENT APPLICATION NURSE: U5/10/218,102
CURRENT FILING DATE: 2002-08-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-798-789-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14; Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.4%; Score 201.5; DB 9; Length 162; illarity 29.8%; Pred. No. 1.3e-08; Conservative 20; Mismatches 72; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-09-10
PRIOR PELICATION NUMBER: US 60/311,545
PRIOR PELICATION NUMBER: US 60/324,899
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/351,937
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 432
SSOFTWARE: PALENTIN VETSION 3.1
SSOFTWARE: PALENTIN VETSION 3.1
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Publication No. US20030130827A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 48; Conserva
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/800,909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE DOCKET NUMBER: WALLACH=12A TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197 TELEPHONE: 202-737-3528 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                 APPLICANT: BELETSKY, IGOR
APPLICANT: BRIT, IGOR
APPLICANT: BRGELWANN, HATUML
TITLE OF INVENTION: TW INHIBITORS
NUMBER OF ESCHORES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                          STREET: 419 Seventh Street, N.W. CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 amino acids
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BIGDA, Jacek
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STRANDEDNESS: si
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Matches 48; Conserv
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US-09-884-987-4
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Sequence 4, Application US/09884987; Patent No. US20020102653A1; GENERAL INFORMATION:

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76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                       DB 9; Length 153;
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE ANTIGEN PILE REPERENCE: 0020-4877P
CURRENT APPLICATION NUMBER: US/09/884,987
CURRENT FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                    19.3%; Score 200.5; DB 9; Length 1 29.8%; Pred. No. 1.5e-08; tive 20; Mismatches 72; Indels
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Job time : 160 secs
                                                                                                                                                                                                                                                                                                                                                                                              48; Conservative
                                                                                                                                                                                       LENGTH: 153
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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: 153 amino acids
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Matches 48; Conservat
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                                                                                                                   June 27, 2005, 14:15:57 ; Search time 42 Seconds (without alignments) 309.260 Million cell updates/sec
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Sequence 3,
                                                                                                                                                                                                                              1 QGGTRSPRCDCAGDFHKKIG......CPTSTLGSCPERCAAVCGWR 174
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Sequence 12
Sequence 12
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.: /cgn2 6/ptodata1/jaa/5A_COMB.pep:*
.: /cgn2 6/ptodata1/jaa/5B_COMB.pep:*
.: /cgn2 6/ptodata1/jaa/6A_COMB.pep:*
.: /cgn2 6/ptodata1/jaa/6A_COMB.pep:*
.: /cgn2 6/ptodata1/jaa/BCMB.pep:*
.: /cgn2 6/ptodata1/jaa/PCTUS_COMB.pep:*
.: /cgn2 6/ptodata1/jaa/PCTUS_COMB.pep:*
              5.1.6
Compugen Ltd.
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US-08-468-560C-4
US-09-800-908-12
US-09-800-908-12
US-09-523-123-53
US-09-523-123-53
US-09-523-087A-10
US-09-855-256A-13
US-09-855-256A-13
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US-09-63-31-35-56
US-08-050-319B-54
US-08-465-982-54
US-09-465-982-2
US-09-855-266A-2
US-09-815-237B-3
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US-08-468-560C-3
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US-09-180-100-9
                                                                                                                                                                                                                                                                                                                     513545 segs, 74649064 residues
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              GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                          US-10-081-280-6_COPY_25_198
1038
                                                                                  protein search, using sw model
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length: 174
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DB seq
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Perfect score:
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APPLICANT: ING, Naoto
APPLICANT: TOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: ADDRESSE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCUNTRY: USA

ZIP: 22202
COMPUTER: EDADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US/07/872,129
FILING APPLICATION NUMBER: US/07/872,129
FILING APPLICATION NUMBER: US/07/872,129
FILING APPLICATION NUMBER: 28,808
REGISTRATION NUMBER: 516762
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TENGTH: TENGTH: 153 amino acids
US-09-180-100-21
US-09-180-100-23
US-09-180-100-23
US-08-08-28-683A-22
US-08-050-319B-2
US-08-465-982-2
US-08-465-982-2
US-08-465-982-4
US-08-465-982-4
US-08-650-319B-5
US-08-650-319B-5
US-08-650-319B-5
US-08-650-319B-5
US-08-650-319B-5
US-08-650-319B-5
US-08-650-319B-5
US-08-853-313-57
US-08-853-313-57
US-08-828-683A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08219237B
Patent No. 5874546
GENERAL INFORMATION:
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76 SOVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 75
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         118 EKQNTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,862
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/476,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US/08/476,862
FILING DATE: 12-OCT-1993
PRIOR APPLICATION NUMBER: IL 194039
FILING DATE: 06-APR-1990
PRIOR APPLICATION NUMBER: IL 91229
FILING APPLICATION NUMBER: IL 91229
FILING BATE: 06-ANG-1989
PRIOR APPLICATION NUMBER: IL 9139
FILING BATE: 18-AMY-1989
ATPLICATION NUMBER: IL 90339
FILING BATE: 18-AMY-1989
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Best Local Similarity 29.8%; Pred. No. 7.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Mismatches
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TWF INHIBITORS NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                         BROWDY AND NEIMARK 419 Seventh Street, N.W.
                                                                                                                      Sequence 3, Application US/08476862 Patent No. 6262239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25,618
                                                                                                                                                                                                                    APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, IGOR
APPLICANT: METT, IGOR
APPLICANT: BROBLMANN, Hartmut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 2
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
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STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                             US-08-476-862-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: 1
STATE:
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                                            68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
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76 SQVALENCSAVADTRCGCKPGWFVEC --- QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72; Indels 21; Gaps
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                                                                                                133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                  133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patemetin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,347
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Pred. No. 7.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Mismatches
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BICAN, Jacek
APPLICANT: BICTSKY, IGOR
APPLICANT: METT, IGOR
TITLE OF INVENTION: TNF LIGANDS
UVMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                           Sequence 12, Application US/08477347
Patent No. 6232446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/115,685
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1L 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/M9-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
STRANDEDNESS: single
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29.8%;
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Best Local Similarity 29.8%
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20004
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Gaps

21;

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STATE: USA
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BELETSKY, IGOR
METT, IGOR
TITLE OF INVENTION: TWF LIGANDS
TNF INHIBITORS
                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
PPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
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Patent No. 6602931
GENERAL INFORMATION:
RAPPLICANT: WALLACH, David
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 153 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                             COMPUTER READABLE FORM:
                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                       20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-800-908-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 19.3%; Score 200.5; DB 3; Length 153; Best Local Similarity 29.8%; Pred. No. 7.7e-11; Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps
                                                                                                                                                                                       APPLICANT: TTOH, Nacto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 11
CORRESPENDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STREET: P.O. BOX 747
CITY: FALLS CHURCH
118 EKQNTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
                                                                                                                                                                                                                                                                                                                                                                                           STALL:
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,560C
FILING DATE: 06-UUN-1995
FILING PATE: 06-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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; Sequence 3, Application US/09800909
; Patent No. 6555111
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETKY, Igor
; APPLICANT: ERGELMANN, Hartmut
                                                                                                    Sequence 4, Application US/08468560C
Patent No. 6270998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-UUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUREHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
REFRENCE/DOCKET NUMBER: 20-4;
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-205-8000
INFORMATION FOR SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 153 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 19.3%; Score 200.5; DB 4; Length : 1 Similarity 29.8%; Pred. No. 7.7e-11; 48; Conservative 20; Mismatches 72; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/800,909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REPERENCE/DOCKET NUMBER: WALLACH=12A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
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76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 GQVEISSCIVDRDIVCGCRKNOYRHYWSENLFQC----FNCSLCLN-GIVH----LSCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yu, Guo-Linard
APPLICANT: Yu, Guo-Linard
APPLICANT: Tu, Guo-Linard
APPLICANT: Tulich, Steven M.
APPLICANT: Tulich, Steven M.
APPLICANT: Zhai, Yifan
APPLICANT: Zhai, Yifan
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFRENCE: 1488.065000C
CURRENT APPLICATION NUMBER: 60/168,380
EARLIER APPLICATION NUMBER: 60/168,380
EARLIER APPLICATION NUMBER: 60/149,326
EARLIER APPLICATION NUMBER: 60/149,657
EARLIER PILING DATE: 1999-03-01
EARLIER PILING DATE: 1999-06-04
EARLIER PILING DATE: 1999-07-06
EARLIER PILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: 60/137,457
EARLIER APPLICATION NUMBER: 60/134,041
EARLIER PILING DATE: 1999-03-11
EARLIER PILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-02-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 154;
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  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/828,683A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.3%; Score 200.5; DB 4; 29.8%; Pred. No. 7.7e-11; ive 20; Mismatches 72;
                                                                                                                                                                                                                                     FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-58p-1996
ATTORILING DATE: 35-58p-1996
ATTORINEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: 91007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
                                                                                                                                                FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 53, Application US/09523323
Patent No. 6635743
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 154 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9881
AMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 29.8%
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 153;
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                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/800,908
FILING DATE: 08-Mar-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
19.3%; Score 200.5; DB 4;
Best Local Similarity 29.8%; Pred. No. 7.7e-11;
Matches 48; Conservative 20; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: TOWNESHIG, KEVIN
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH=10
                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-800-908-12
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/477,347
FILING DATE: «UNKNOWN»
APPLICATION NUMBER: 11 106271
FILING DATE: 08-JUL-1993
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CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ 1D NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
NUMBER OF SECUENCES: 17
                                                                                                                                                               ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                           COUNTRY: USA
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76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                     16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 75
                                                                                                                                                                                                                                                                                                              Length 161;
                                                                                                                                                                                                                                                                                                                                                           72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                            19.3%; Score 200.5; DB 3; 29.8%; Pred. No. 8.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-232-087A-10

Sequence 10, Application US/08232087A

Patent No. 5866372

GENERAL INFORMATION:

APPLICANT: Stein, Harald
APPLICANT: Latza, Ute
APPLICANT: Latza, Ute
TITLE OF INVENTION:

TITLE OF INVENTION: Lymphoid CD30-Antigen
NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,087A
FILING DATE: 08-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFRENCE/DOCKET NUMBER: 756-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
                      ATTORNEY/AGENT INFORMATION:
NAME: Zindrick, Thomas K.
REGISTRATION NUMBER: 32,185
REFERENCE/DOCKET NUMBER: A-4
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
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                                                                                                                                                                   : 161 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                           48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s. protein
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                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-09-326-394-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
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                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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  FILING DATE:
                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC-----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 75
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 19.3%; Score 200.5; DB 4; Length 154; Best Local Similarity 29.8%; Pred. No. 7.7e-11; Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sendele, Alison M.
APPLICANT: Sendele, Regina M.
APPLICANT: Sendello, Regina M.
APPLICANT: Sedwards, Carl K.
TITLE OF INVENTION: COMBINATION THERAPY USING A TWF BINDING
TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES
CORRESPONDENCE AMGEN INC.
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 EKONTVCTCHAGPFLRENECVSC----SNCKKSLECTKLC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRILLAR: ALTERN: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/326,394
FILING DATE: 08-DEC-1997
                   EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/003,886
EARLIER APPLICATION NUMBER: 08/822,953
EARLIER FILING DATE: 1998-01-07
EARLIER FILING DATE: 1999-03-21
EARLIER FILING DATE: 1996-03-22
EARLIER FILING DATE: 1996-03-22
EARLIER FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO S: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/032,587
FILIND DATE: 06-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,355
FILIND DATE: 23-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION
EARLIER APPLICATION NUMBER: 09/027, 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 60/052,023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09326394
Patent No. 6306820
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-523-323-53
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                                                                                                                                                                                                                        9 HPQNNSICCTKCHKGTYLYNDCPGPGPGDTDCDECESOSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                              16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 75
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                                                                                                                                                        Gaps
                                                                                                                                                   Indels 21;
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                                                                                                             Length 154;
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                                                                                                                                                                                                                                                                                                                                                                   133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13. Application US/09855266A
Patent No. 6784284
GENERAL INFORMATION:
APPLICANT: Kimura, Naoki
APPLICANT: Toyoshima, Tomoko
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE RERENCE: 06501-040002
CURRENT APPLICATION NUMBER: US/09/855,266A
                                                                                                      Query Match 19.1%; Score 198.5; DB 2; Best Local Similarity 30.4%; Pred. No. 1.2e-10; Matches 49; Conservative 23; Mismatches 68;
                                        /note= "TNFR1, see Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lacey, William
APPLICANT: Lacey, David
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 RRDTDCGTCLPGFYEHGDGCVSC 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 31.5%
Matches 45; Conservative
               LOCATION: 1..154
CTHER INFORMATION:
US-08-232-087A-10
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ORGANISM: Homo sapiens
US-08-706-945D-129
NAME/KEY: Protein
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Sequence 4, Application US/09146950A

Sequence 4. Application US/09146950A

GENERAL INFORMATION:

APPLICANT: BUSIFIELD, Samantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED

TITLE OF INVENTION: PROTEIN PAMILY AND USES THEREOF

FILE REFERENCE: 09404/05701

CURRENT APPLICATION NUMBER: US/09/146,950A

CURRENT FILING DATE: 1998-09-03

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 QACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTR 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CPGGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLR-QCLSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 CAGD -- FHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 KTCRKEMSQVEISPCQADKDTVCGCK----ENQFQRYLSETHFQC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 -----VDCSPCF-----NGTVTIP-----CKETONTVC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 LLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPERCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.8%; Score 185; DB 4;
28.8%; Pred. No. 1.5e-09;
tive 16; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 RDTDCGTCLPGFYEHGDGCVSCPTSTLGSC 163
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CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 09/411,722
PRIOR PILING DATE: 1999-10-01
PRIOR PILING DATE: 1998-04-01
PRIOR PELING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: JP 9/099653
PRIOR FILING DATE: 1997-04-01
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
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'Sequence 20' Application US/09146950A

'Patent No. 6287808

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Conservative
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                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 46; Conser
                                                                                                                                                                                                                                                                                                                                                                                                  US-09-855-266A-13
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LENGTH: 155
TYPE: PRT
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APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: NOVEL MOLECTLES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REPERENCE: 09404/057001
CURRENT APPLICATION NUMBER: 18/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 159
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Pacent No. 6635743

GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Ruben, Steven M.
APPLICANT: Suber, Reinhard
APPLICANT: Tu, Guo-Liang
APPLICANT: Ullrich, Stephen
CURRENT APPLICATION NUMBER: US/09/523,323
CURRENT APPLICATION NUMBER: 60/148,326
EARLIER APPLICATION NUMBER: 60/148,326
EARLIER APPLICATION NUMBER: 60/14,657
EARLIER APPLICATION NUMBER: 60/14,657
EARLIER APPLICATION NUMBER: 60/14,657
EARLIER APPLICATION NUMBER: 60/14,041
EARLIER APPLICATION NUMBER: 60/13,457
EARLIER APPLICATION NUMBER: 60/13,457
EARLIER APPLICATION NUMBER: 60/13,457
EARLIER APPLICATION NUMBER: 60/015,409
EARLIER PILING DATE: 1999-02-19
EARLIER APPLICATION NUMBER: 09/02,20
EARLIER APPLICATION NUMBER: 09/03,20
EARLIER APPLICATION NUMBER: 09/03,03
EARLIER APPLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 IGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHN--SECARCOACDEQAS 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.5%; Score 182; DB 3; 30.7%; Pred. No. 3.7e-09; ative 14; Mismatches 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 30.7%;
46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-09-146-950-20
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Compugen Ltd.
GenCore version
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- protein search, using sw model OM protein June 27, 2005, 14:31:28 ; Search time 38 Seconds (without alignments) 202.562 Million cell updates/sec Run on:

US-10-081-280-6_COPY_338_417 Title: Perfect score:

1 VMDAVPARRWKEFVRTLGLR......ERMGLDGCVEDLRSRLQRGP Sequence:

80

Scoring table:

Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

26016 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 80 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote		hypothetical prote		hypothetical prote	hypothetical prote	-	hypothetical prote	hypothetical prote	unknown protein, 7	hypothetical prote	repressor protein	probable damage-in	hypothetical prote		hypothetical prote	OI	~	-		host factor for ly	slyX protein - Esc	hypothetical prote	probable phage tai	keratin 15, type I	hypothetical prote	hypothetical prote	e	hypothetical prote
SUMMARIES		F71080	G69463	E69386	D69499	A84092	H84353	A82881	D83610	C69333	A96702	G83940	JH0129	AH0619	A75099	H70576	F83985	AC1037	H70799	F72303	G91153	C85999	A49988	B75199	AG0927	B55682	F81899	F69871	AE2659	C97441
	03	7	~	~	~	~	~	~	~	~	~	7	N	~	~	N	0	~	Н	N	~	~	~	N	~	~	~	N	N	7
	Query Match Length	74	71	72	73	79	78	72	9	61	67	64	68	79	72	16	25	67	71	80	72	72	72	74	67	68	70	62	75	75
a	Query Match	12.7	12.2	12.2	12.2	12.2	12.0	11.6	11.4	11.4	11.4	11.3	11.3	11.3	11.1	11.1	11.0	10.9	10.9		10.8	10.8	٠	10.8	10.7	10.7	•		10.5	10.5
	Score	1	50.5	50.5	50.5		49.5	48	47	47	47	46.5	46.5	46.5	46	46	45.5	45	45	45	44.5	44.5		44.5	44	44	44	٠	43.5	43.5
	Result No.	-	7	٣	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

probable ribosomal	Icd-like protein [hypothetical prote	ribosomal protein	hypothetical prote	conserved hypothet	mineralocorticoid	M protein precurso	hypothetical prote	hypothetical prote	M protein precurso	conserved hypothet	hypothetical prote	hypothetical prote	50S ribosomal prot	hypothetical prote	
E70644	A90826	H81238	T45384	F64547	F69219	153270	860803	A82086	F72592	860835	D69283	AD2769	нв3960	D81212	C69327	ALIGNMENTS
~	~	~	~	~	~	~	~	~	~	c	~	N	N	~	N	
65	65	65	71	73	77	47	28	77	79	80	37	61	73	77	36	
10.4	10.4	10.4	10.4	10.4	10.4	10.3	10.3	10.3	10.3	10.3	10.2	10.2	10.2	10.2	10.0	
43	43	43	43	43	43	42.5	42.5	42.5	42.5	42.5	42	42	42	42	41.5	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

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Cipacies: Pyrococus borikoshi;
Cipacies: Pyrococus borikoshi;
Cipacies: Pyrococus borikoshi;
Cipacies: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
CiAccession: F71080
R:Rawarabayash; Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekink
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res 5, 55-76, 1998
A.; Seference and gene organization of the genome of a hyper-thermophilic an
A.Reference number: A71000; MUID:98344137; PMID:9679194
A.; Reference number: A71000; MUID:98344137; PMID:98336131; PIDN:BAA30004.1; PID:d1036
A.; References: UNIPROT:073992; GB:AP000004; NID:93236131; PIDN:BAA30004.1; PID:d1036
A; Rose: references: UNIPROT:073992; GB:AP00004; NID:93236131; PIDN:BAA30004.1; PID:d1036
A; Rose: references: UNIPROT:073992; GB:AP00004; NID:93236131; PIDN:BAA30004.1; PID:d1036
A; Rose: References: UNIPROT:073992; GB:AP00004; NID:93236131; PIDN:BAA30004.1; PID:d1036
A; Rose: PHS027
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hypothetical protein PHS027 - Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.7%; Score 52.5; Dilarity 27.3%; Pred. No. 82; Conservative 14; Mismatches
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hes 18; Conservat
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67 VEGMKE 72
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Matches
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RESULT 2 G69463

Conserved hypothetical protein AF1712 - Archaeoglobus fulgidus
Cipace: Archaeoglobus fulgidus
Cipace: Archaeoglobus fulgidus
Cipace: Ob-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cipacesion: G69463
Rixlenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A;Title: The preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-71 <KLE>

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Conserved hypothetical UU518 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Useaplasma urealyticum C;Accession: A82881 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to Gensamk, February 2000 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min; A;Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: DNA
A,Residues: 1-79 <STO>
A,Cross-references: UNIPROT:Q9K736; GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB072:
A,Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Vng2035h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Accession: H84153
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H., Alam, M.; Freitas, T. 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liż
A;Ritle: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
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C;Genetics:
                                                                                                                                                                                                                  F.; Hiran
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hypothetical protein BH3537 [imported] - Bacillus halodurans (strain C-125) (Species: Bacillus halodurans C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Accession: A84092 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Ree. 28, A311-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
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12.2%; Score 50.5; DB 2;
Best Local Similarity 27.6%; Pred. No. 1.4e+02;
Matches 16; Conservative 12; Mismatches 15;
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Matches 15; Conservative
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A; Residues: 1-72 <GLA>
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A; Status: preliminary
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Matches
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Cispecies: Archaeoglobus fulgidus
Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_chum, K.A.; Dodson
FixIdenk, H.B.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
Cipate: Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.
Clodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
Alauthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Authors: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A69250; MUID:98049343; PMID:9389475
     A;Cross-references: UNIPROT:028561; GB:AE000985; GB:AE000782; NID:g2689308; PIDN:AAB8953
C;Superfamily: Methanococcus jannaschii hypothetical protein MJ0975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: D69499
R; Klenk, H.D.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
: Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Gloddk, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Astutores 390, 364-370, 1997
A; Authores: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A; Reference number: A69250; MUID:98049343; PMID:9389475
A; Status; preliminary; nucleic acid sequence not shown; translation not shown
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Superfamily: uncharacterized conserved protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein AF1997 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                           Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                      4 IIEAVYQKGVLKPLRKVSLREGEIVKVEIRETKKVTGRFYAKLRELEKR
                                                                                                                                                                                                                                                                                                                                          1 VMDAVPARRWKEFVRTLGLREAEIEAVEVE----IGRFRDQQYEMLKR
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                                                                                                                                                 Query Match
12.2%; Score 50.5; DB 2;
Best Local Similarity 32.7%; Pred. No. 1.3e+02;
Matches 16; Conservative 10; Mismatches 18;
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Best Local Similarity 27.8*
Matches 15; Conservative
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Mon Jun 27 14:58:46 2005

11.6%; Score 48; DB 28.0%; Pred. No. 2.4e iive 10; Mismatches

Query Match Best Local Similarity 28.0* Matches 7; Conservative

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A;Gene: UU518 A;Genetic code: SGC3

| :::||| : :::||:| EYIKTLGRNONAVVYIQTKDGKFQD 65 12 EFVRTLGLREAEIEAVEVEIGRFRD 36

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; W., D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Atile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CiAccession: G83940
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acida Rea: 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and ç A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83940
A;Status: preliminary
A;Residues: 1-64 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q9KAGO; GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB0604
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2327
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N.Alternate names: repressor protein F
C;Species: Bacherichia coli
A;Note: plasmid RSF1010 is a broad-host-range plasmid belonging to incompatibility group
A;Note: plasmid RSF1010 is a broad-host-range plasmid belonging to incompatibility group
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Ju1-2004
C;Accession: JH0129; PS0292
R;Scholz, P: Hating, V.; Wittmann-Liebold, B.; Ashman, K.; Bagdasarian, M.; Scherzinger,
R;Scholz, P: Jazing, V.; Wittmann-Liebold, B.; Ashman, K.; Bagdasarian, M.; Scherzinger,
A;Title: Complete nucleotide sequence and gene organization of the broad-host-range plasm
A;Reference number: JH0123; MUID:89232758; PMID:2653965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-67 <STO>
A;Cross-references: UNIPROT:Q9C9V8; GB:AE005173; NID:g6553903; PIDN:AAF16569.1; GSPDB:GN(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 KEF--VRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 2; Length 67;
Pred. No. 2.9e+02;
5; Mismatches 13; Indels
unknown protein, 70659-70456 [imported] - Arabidopsis thaliana
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34.8%;
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Matches 16; Conservative
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A; Status: preliminary
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Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-60 cSTO>
A;Cross-references: UNIPROT:Q916KG; GB:AE004466; GB:AE004091; NID:g9946120; PIDN:AAG0367
A;Experimental source: strain PAO1
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                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein PA0284 [imported] - Pseudomonas aeruginosa (strain PAO1) C.Species: Pseudomonas aeruginosa C.Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C.Accession: D83610
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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                                                                    ; DB 2; Length...
2.4e+02;
8; Indels
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Score 47; DB 2; Length 60; Pred. No. 2.6e+02; 6; Mismatches 15; Indels

ch 11.4%; 1 Similarity 36.4%; 12; Conservative (

Best Local Similarity Matches 12: Consery

A; Gene: PA0284

Genetics:

19 LREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPA

ઠ ద 11.4%; Score 47; DB 2; Length 61; 34.5%; Pred. No. 2.6e+02;

12; Indels

7; Mismatches

10; Conservative

Matches

RESULT 10 A96702

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Best Local Similarity

Query Match

35 RDQQYEMLKRWRQQQPAGLGAVYAALERM 63 ||:: ||:| :||: RDEKLRMLERMRDELEAELEEIKREIERL

A; Accession: JH0129

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Search completed: June 27, 2005, 14:41:37 Job time : 40 secs
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6. Species: Salmonella enterica subsp. enterica serovar Typhi
6. Note: this species has also been called Salmonella typhi
6. Dave-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
6. Accession: AH0619
7. Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seroval A; A; Accession: AH0619
                                                A;Cross-references: UNIPROT:Q52350; GB:M28829; NID:g152577; PIDN:AAA26449.1; PID:g152585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: A75099
                                                                                                   A;Molecule type: protein
A;Residues: 1-18 <SCH2>
C;Comment: This protein binds to the operator region of a promoter located at upstream
                                                                                                                                                                                                                                                                                                                                           7
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                                                                                                                                                                                                                                                                                                                                                                                        3 DAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALER 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 RTLGLREAEIEAVEVEIGRFRDQQYE----MLKRWRQQQPAGLGAVYAALERMGLDGCVE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C'Species: Pyrococcus abyssi
C'Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.3%; Score 46.5; DB 2; Length 79;
32.8%; Pred. No. 3.9e+02;
tive 8; Mismatches 24; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                        15; Indels 31; Gaps
                                                                                                                                                                                                                                                                               Query Match 11.3%; Score 46.5; DB 2; Length 68; Best Local Similarity 20.8%; Pred. No. 3.3e+02; Matches 15; Conservative 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein PAB3293 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 32.89
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 MGLDGCVEDLRS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----CLEELRA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 DLRSRLQ 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIQŠIĽO 66
A; Molecule type: DNA
A; Residues: 1-68 <SCH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-79 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Status: preliminary
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A,Molecule type: DNA
                                                                           A; Accession: PS0292
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                                                                                                                                                                                                                                  A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Gene: STY1032
                                                                                                                                                                                                         A;Gene: cac
                                                                                                                                                                              C, Genetics:
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Pypothetical protein Rv2132 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Species: Mycobacterium tuberculosis

C;Accession: H70576

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

R;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome FA;Reference number: A70500; MUID:98295987; PMID:9634230
A;Cross-references: UNIPROT:09UZG5; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50094
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB3293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:006243; GB:295388; GB:AL123456; NID:g3261759; PIDN:CAB08638.1
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                 ij
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 RSIGLSEAVNELIRAGLTKRQVANRFQQQTYDM------GEGIDYSNIGDAIET-- 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 RTLGLREAEIEAVEVEI-----GRFRDQQYEMLKRWRQQQPAGLGAVYA----ALERMG
                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                         Length 72
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                  11.1%; Score 46; DB 2;
38.7%; Pred. No. 4e+02;
ive 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     14 VRTLGLREAEIEAVEV--EIGRFRDQQYEML 42
                                                                                                                                                                                      Query Match
Best Local Similarity 38.73
Matches 12; Conservative
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Pseudomonas putida.
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22; Conserv
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NCBI_TaxID=303;
Name=rpoS;
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Best Local 3
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Matches
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Q6TG30
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Q93R97
HA HA
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Q7b21 fusobacteri
Q2x19 bacteriopha
Q6czu0 erwinia car
Q8Lya5 methanopyru
Q72gh9 thermus the
Q8u39 pyrococcus
Q719x2 synechococc
Q9145 oryaz sativ
Q747 prochloroco
Q9171 archaeoglob
Q29171 archaeoglob
Q29171 archaeoglob
Q29171 archaeoglob
Q29171 archaeoglob
Q29171 archaeoglob
Q29736 bacillus ha
Q8d62 vibrio vuln
Q8rx2 sativ
Q7by vibrio para
Q8d62 vibrio vuln
Q8rx3 dinglymosto
Q8cx2 shewanella
Q8rx5 cryza sativ
Q8rx5 vibrio vuln
Q8rx5 vibrio vuln
Q8rx9 cryza sativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293r97 pseudomonas
                                                                                                               (without alignments)
243.847 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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                                                                                                June 27, 2005, 14:30:44 ; Search time 168 Seconds
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            5.1.6
Compugen Ltd.
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            GenCore version (c) 1993 - 2005
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YA94 ARCFU
YJ97 ARCFU
Q9K736
Q8DD62
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Maximum Match 100%
Listing first 45 summaries
                                                                      protein search, using sw model
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Q6TG30
Q7P3Z1
Q9ZXL9
Q6CZU0
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Q8H4R5
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Q6PXY4
Q93NF5
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Q8ECW2
Q87PB4
Q9HNM4
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Q72GH9
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Q7EYN4
Q7V7D7
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Q7MKX6
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Gapop 10.0 , Gapext 0.5
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Q883A4
Q716N0
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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EMBL; AB054812; Belongs to the sigma-70 factor family.

BRBL; AB054812; BAB62001.1; -.

RSP; QBEZUB; IKU3.

RO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.

GO; GO:0015987; F:sigma factor activity; IEA.

GO; GO:0015700; F:transcription factor activity; IEA.

RO; GO:0005700; F:transcription factor; IEA.

GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:000535; P:regulation of transcription, IEA.

RO; GO:000535; P:regulation of initiation; IEA.

RO; GO:000535; P:regulation initiation; IEA.

RINTEFPRO; IPRO0043; Sigma-70.

R InterPro; IPRO0043; Sigma-70.

R Pfam; PF04545; Sigma-70.

R PROSITE; PS00716; SIGMA-70.

R PROSITE; PS00716; SIGMA-70.

R Transcription regulation; Transferase.
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Q8wti4 aretaon asp
Q8wtf1 timema knul
                                                                  arabidopsis
                                                                                        giardia lam
staphylococ
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                                                                                                                                                                                                                                          timema knul
phyllium bi
                         hyposoter drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohmori D.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: Sigma factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are then released (By similarity).
-- SIMILARITY: Belongs to the sigma-70 factor family.
-- EMBL; AB054812; EAB62001.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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    09ppx1
06q6g0
024410
06nnn4
07r0h4
06pxy6
06pxy7
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SEQUENCE 79 AA; 9136 MW; AE74B2F1226CC213 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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OGTG30;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA polymerase sigma factor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Q9PPX1
Q6Q6G0
Q24410
Q6DNN4
Q7R0H4
Q6PXY7
Q8WTH4
Q8WTH4
Q8WTG4
Q8WTG4
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Q93R97;
01-DEC-2001 (TEMBLrel. 19,
01-DBC-2001 (TEMBLrel. 19,
01-MAR-2004 (TEMBLrel. 26,
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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SEQUENCE FROM N.A.
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                                                                                                                                                     Bacteriophage phi
                                                                                                                                                                                               NCBI_TaxID=35343;
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01-MAR-2004
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25-OCT-2004
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                                RESULT 4
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Q6CZU0
                                              ð
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                                                                                                                                         A Scott A., Meakins D., Page W.J.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

Li Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

I FUNCTION: Signa factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are then released (By similarity).

Li SIMILARITY: Belongs to the sigma-70 factor family.

EMBL; AV42193; AAS90415.1; ...

GO; GO:0016987; F:signa factor activity; IEA.

GO; GO:0016987; F:signa factor activity; IEA.

GO; GO:0016555; F:regulation of transcription, DNA-dependent; IEA.

GO; GO:0016555; P:transcription initiation; IEA.

InterPro; IPR007630; Sigma-70.

R InterPro; IRR007630; Sigma-70.

R PRINTS; PR00046; Sigma-70.

R PRINTS; PR00046; SIGMA70FCT.

PROSITE; PS00716; SIGMA70FCT.

M DNA-binding; DNA-directed RNA polymerase; Sigma factor; Transcription;

M DNA-binding; DNA-directed RNA polymerase; Sigma factor; Transcription;

M DNA-binding; DNA-directed RNA polymerase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 VRTLGLREAE---IEAVEVEIG----RFRDQQYEMLKRWRQQQPAGLGAVYAALERMGL
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Karpatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A., Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T., Gardner W.L., Wikhailova N., Kyrpides N.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
-: CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                         Azomonas macrocytogenes.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azomonas.
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Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Indels
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Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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,, AABF01000154; EAA23321.1; -.
FENCE 59 AA; 6808 MW; 615C5DF19B318E86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                55 AA; 6365 MW; 7476036EFCE12854 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.8%; Score 57; DB 2; I
39.0%; Pred. No. 1.3e+02;
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               Stationary phase sigma factor (Fragment)
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01-MAR-2004 (TrEMBLrel. 26, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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ilarity 37.2%;
Conservative
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nes 16; Conserv
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                                                                                                                                   STRAIN=ATCC 12334;
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                                                                                                                   SEQUENCE FROM N.A.
                                                                                       NCBI_TaxID=69962;
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STRAIN=phiCTX-c; MEDLINE=90014160; PubMed=2507866; MEDLINE=90014160; PubMed=2507866; Hayashi T., Kamio Y., Hishinuma F., Usami Y., Titani K., Terawaki Y.; Hayaudomonas aeruginosa cytotoxin: the nucleotide sequence of the gene and the mechanism of activation of the protoxin.";
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PubMed=15263089; DOI=10.1073/pnas.0402424101;
PubMed=15263089; DOI=10.1073/pnas.0402424101;
Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
"Genome sequence of the enterobacterial phytopathogen Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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"The complete nucleootide sequence of phiCTX, a cytotoxin-converting phage of Peudomonas aeruginosa: implications for phage evoltion and horizontal gene taransfer via bacteriophage.";
Mol. Microbiol. 31:399-419(1999).
BMBL; AB008550; BAA36234.1;
Interpro; IPR00861; Tail X.
Pfam; PF05489; Phage tail X;
SEQUENCE 69 AA; 7436 MW; DZE35A698F195CC0 CRC64;
                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
P2-like viruses.
                                                                       01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Pseudomonas aeruginosa phage phi CTX, complete genome sequence.
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Pred. No. 3.5e+02;
4; Mismatches 9; Indels
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EMBL; BX950851; CAG76958.1; -.
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Last annotation update)
69 AA.
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                                                  Created)
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MEDLINE=99157549; Pubmed=10027959;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Microbiol. 3:861-868(1989)
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PRELIMINARY;
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                                               (TrEMBLrel.
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Pyrococcus furiosus
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 WCBI_TaxID=262724;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2261;
                                      PubMed=15064768;
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01-OCT-2003
                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                    Methanopyrus kandleri.
Archaea; Buryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens.";
Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
OrderedLocusNames=TTC1869;
Thermus thermophilus (Errain HB27 / ATCC BAA-163 / DSM 7039)
Bacteria; Deinococcus Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                   12;
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                                                                                                                                                                      1 MIIPWQQLDPETLDSIIESFVLREGTDYGEQER-SLAQKVEDIRSQLQSG 49
                                                                                                                                             41 MLKRWRQQQPAGL-----GAVYAALERMGLDGCVEDLRSRLQRG
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                                                                                          Length 78;
                                                                                                                   16; Indels
                                                                                                                                                                                                                                                                    01-OCT-2003 (TrEMBLrel. 21, Last sequence update)
Predicted RNA-binding protein containing the S4 domain.
Methanonvrie
                                                  Complete proteome, Hypothetical protein.
SEQUENCE 78 AA; 8894 MW; CC29D8DC6F12BF9C CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                         13.1%; Score 54; DB 2; llarity 36.0%; Pred. No. 4e+02; Conservative 4; Mismatches 1.
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            InterPro; IPR010648; UPF0270.
Pfam; PF06794; UPF0270; 1.
PIRSF; PIRSF006169; UCP006169; 1.
 InterPro; IPR008227; UCP006169.
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PROSITE; PS50889; S4; 1.
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SEOUENCE 79 AA;
                                                                                                    Best Local Similarity
Matches 18; Conserv
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Henne A., Brueggemann H., Raasch C., Wiezer A., Hartsch T., Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R., Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber R., Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.; "The genome sequence of the extreme thermophile Thermus thermophilus.";
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Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE010180; AAL80697.1; --
Pfam; PF04014; SpoyT AbrB; 1.

TIGRFAMS; TIGR01439; lp_hng_hel_AbrB; 1.
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                                                                                                                                                                                                                                                                                                             12.8%; Score 53; DB 2; Length 62; 29.3%; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                            Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                           Nat. Biotechnol. 22:547-553(2004).
EMBL, AE017307; AAS8211.1;
Complete protecome; Hypothetical protein.
SEQUENCE 62 AA; 7921 MW; 0D272F18D427D6EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 AA; 8705 MW; 6FE2F4AF7D807146 CRC64;
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les 17; Conservative 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=PF0573;
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Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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  Pyrococcus horikoshii.
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Best Local Similarity
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                                                           NCBI_TaxID=53953;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
45-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypochetical protein OJ1457_D07.108 (Hypothetical protein OJ1058 B11.129).
Name=OJ1457_D07.108; Synonyms=OJ1058 B11.129;
OYZA BALIVA (Japonica Cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                   2;
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Best Local Similarity 31.7%; Pred. No. 5.2e+02;
Matches 19; Conservative 8; Mismatches 28; Indels
                                                                                                                                                                                                                                                                       Length 78;
                                                                                                                                                                                                                                                                   Query Match
12.8%; Score 53; DB 2; Length 78;
Best Local Similarity 34.1%; Pred. No. 5.1e+02;
Matches 14; Conservative 14; Mismatches 11; Indels
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EMBL; AP003956; BAC21370.1; -.
EMBL; AP003864; BAD30405.1; -.
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                    36 DQQYEMLKRWRQQQPAGLGAVY-AALERM-GLDGCVEDLRS 74
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Hypothetical protein.
SEQUENCE 70 AA; 7543 MW; 43E9E837A80B9238 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UDV-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PHS027.
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NCBI_TaxID=84588;
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MEDLINE=98344137; PubMed=9679194;

Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,

Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,

Askai M., Ogura K., Osuka B.-I., Kosugi H., Hosoyama A., Nagai Y.,

Bakai M., Ogura K., Osuka R., Nakazawa H., Takamiya M., Ohfuku Y.,

Punahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,

Masuchi Y., Shizuya H., Kikuchi H.;

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thermophilic archaebacterium, Pyrococcus horikoshii OT3.";

DNA Res. 5:55-76[1998].

EMBL, Ap000004; BAA30004.1; -.

RISP: PO8074; IERT.

RISP: PR0063139; AbrB trans_reg.

RICEPPO: IPR0063139; AbrB trans_reg.

RICEPPO: IPR00159; SpovT AbrB;

RICEPPO: IRRON159; SpovT AbrB;

RICEPPO: ITGRPMS; ITGR01439; lp_hng_hel_AbrB; 1.
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Last annotation update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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Hypothetical protein.
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[7]
SEQUENCE FROM N.A.
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05-JUL-2004 (
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01-JUN-2003
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Best Local (
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MEDLINB=21405725; PubMed=11514508;

MEDLINB=21405725; PubMed=11514508;

DOI=10.1128/1918.18.5262-567.2001;

Baitsch D., Sandu C., Brandsch R., Igloi G.L.;

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J. Bacteriol. 183:5262-5267(2001).
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Bottcher B., Brandsch R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schenk S., Hoelz A., Kraus B., Decker K.;
"Gene structure and properties of enzymes of the plasmid-encoded nicotine catabolism of Arthrobacter nicotinovorans.";
J. Mol. Biol. 284:1323-1339 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97230479; PubMed=9073580; DOI=10.1006/plas.1996.1272; Menendez C., Igloi G.L., Brandsch R.; "IS1473, a putative insertion sequence identified in the plasmic from Arthrobacter nicotivorans: isolation, characterisation and distribution among Arthrobacter species."; Plasmid 37:35-41(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLASMID=pAO1;
MEDLINE=99096870; PubMed=9878353; DOI=10.1006/jmbi.1998.2227;
 64
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                                                                                                                                                                          Plasmid pA01, and Plasmid pA01.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Micrococcaceae; Arthrobacter.
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Grether-Beck S., Igloi G.L., Pust S., Schiltz E., Decker K.,
              LGLREAEI EAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMG
                                                                                                                            Last sequence update)
Last annotation update)
                                                                                      70 AA
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MEDLINE=96172783; PubMed=8588735;
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                                                                                                                                                                Arthrobacter nicotinovorans
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                                            DOI=10.1128/JB.185.6.1976-1986.2003;
Igloi G.L., Brandsch R.;
"Sequence of the 165-kilobase catabolic plasmid pAOI from Arthrobacter
"Sequence of the 165-kilobase catabolic plasmid pAOI from Arthrobacter
nicotinovorans and identification of a pAOI-dependent nicotine uptake
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Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
Madupu R., Daudgherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
Bender C.L., White O., Fraser C.M., Collmer A.;
The complete genome sequence of the Arabidopsis and tomato pathogen
Pseudomonas syringae pv. tomato DG3000.";
Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
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Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
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Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                              Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                   23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Indels
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                                                                                                                                                                                                          EMBL, AF373840, AAK64270.1; -.
EMBL, AJ507836; CAD47929.1; -.
Hypothetical protein; Plasmid.
Hypothere 70 AA, 7833 MW, 1501DDE147F444FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protecme; Hypothetical protein.
66 AA; 7274 MW; 6DD44F84FA4A630C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 RDDOWTWIGRMTDLPPSGLGLCQAADTKGGRCLCVNKSHCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 RDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSR
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(TrEMBLrel. 27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                 Score 52; DB 2; Pred. No. 5.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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PLASMID=pAO1;
MEDLINE=22505657; PubMed=12618462;
                                                                                                                                                       system.";
J. Bacteriol, 185:1976-1986(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                 12.6%;
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nes 15, Conservative
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12.2%; Score 50.5; DB 2; Length 63;
Best Local Similarity 32.8%; Pred. No. 7.6e+02;
Matches 21; Conservative 8; Mismatches 20; Indels 15; Gaps
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein OSJNBb0011E04.106.
Name=OSJNBb0011E04.106;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
NCBL TaxID=39947;
                                                                                                                                              [1] --
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUBMILT ., Matsumoto T., Katayose Y.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005443; BAD05624.1; -.
Hypotherical protein.
SEQUENCE 63 AA; 7063 MW; 348C125AE42F427D CRC64;
          8 6
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Search completed: June 27, 2005, 14:40:56 Job time : 174 secs

59 ALER 62 |: | 60 AVRR 63

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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG31492;
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Apo-3/DR3
Human Apo
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Death dom
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Chlamydia
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Human DR4
                                                                                         June 27, 2005, 14:22:33 ; Search time 158 Seconds (without alignments) 195.828 Million cell updates/sec
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Ada49709 1
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                      2105692 segs, 386760381 residues
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Maximum Match 100%
Listing first 45 summaries
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ADG40452
ADA49713
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AAB26990
AABG31493
ADG49709
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AAB26992
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ADO40453
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geneseqp2003bs:*
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Match Length
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67
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Aae38911 Chlamydia Aaw62177 Nerve gro Ad125858 Nerve gro	Aawo0206 Human Fas Aaw93611 Human Fas Aab26988 Human CD9	Aam80357 Human hae Abg31494 Human Apo Ada49710 Death dom	Adg98746 Fas/Apol Ado40455 Human Fas Ase24866 Chlamydia		Adn46273 Thermococ Aae24856 Chlamydia Aae38899 Chlamydia	Aau63529 Propionib Abm60048 Propionib
5 AAE38911 2 AAW62177 8 ADJ25858	2 AAW00206 2 AAW93611 3 AAB2698		7 ADG98746 8 ADO40455 5 AAE24866	5 AAE38909 5 AAE24857 5 AAE38900	8 ADN46273 5 AAE24856 5 AAE38899	4 AAU63529 6 ABM60048
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64.5 15.6 60 14.5 60 14.5	ก้เก้	7.5 13. 7.5 13. 7.5 13.	57.5 13.9 57.5 13.9 57 13.8	57 13. 57 13. 57 13.	56.5 13.7 56 13.6 56 13.6	55 13.3 55 13.3
24 24 28	29 30 31	3 3 3 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	35 36 37	338 409	4 4 4 4 3 2 3	44 5

ALIGNMENTS

Human Apo-2DcR associated protein #2 ABG31492 standard; protein; 74 AA (first entry)

Human, Apo-2DCR, Apo-2 ligand, programmed cell death, apoptosis, neurodegenerative disease; autoimmune, inflammatory.

21-JUN-2001; 2001US-00887879. 97US-0049911P. 98US-00096500.

Kim KJ; Gurney A, Chuntharapai A, Ashkenazi AJ, Baker KP,

Novel isolated Apo-2DcR polypeptide useful for modulating apoptosis in

Disclosure; Page 37; 58pp; English

The present invention relates to the isolation of novel human polypeptides, designated Apo-2DCR, and the polynucleotide sequences encoding them. Apo-2DCR is capable of binding Apo-2 ligand and is useful for modulating programmed cell death or apoptosis in mammalian cells. Apo-2DCR can be used to produce apo-2DCR antibodies which are useful therapeutically, and can cross-react with other receptors for Apo-2 ligand to block excessive apoptosis in neurodegenerative diseases, or to block potentially autoimmune or inflammatory effects. Apo-2DCR antibodies are also useful in immunohistochemistry staining assays or diagnostic assays for Apo-2DCR, e.g. detecting it's expression in specific cells, tissues or serum, and for the affinity purification of Apo-2DCR from recombinant cell culture or natural sources. The present sequence

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74

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1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAAL 60
                        61 ERMGLDGCVEDLRS
                                      ERMGLDGCVEDLRS
                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-090468/09.
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Best Local Similarity
                                                                                                                                                                                                                                           JS2004009552-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 74 AA;
                                                                                                                                                                                                                                                                                                                             14-MAY-1998;
02-NOV-2001;
06-NOV-2002;
                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                             15-JUL-2004
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09-FEB-1998;
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                                                                                                                                                                                                                                                                                                                   Apo-2; apoptosis; diagnosis; tissue-specific typing; transgenic animal;
  to the present
the Seq listing but
                                                                                                            VMDAVPARRWKEFVRTLGLREAEIBAVBVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAAL
                                                                                                                               1 VMDAVPARRWKEFVRTLGLREAEIBAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAAL
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Apo-2 polypeptide or its extracellular or death domain sequence, useful for modulating apoptosis in mammalian cancer cells or for generating transgenic or knockout animals.
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0
                                                                92.3%; Score 381; DB 5; Length 74; 100.0%; Pred. No. 5e-41; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.3%; Score 381; DB 7; Length 74; 100.0%; Pred. No. 5e-41; tive 0; Mismatches 0; Indels
represents a protein of unknown function relating invention. Note: The present sequence is given in not mentioned elsewhere in the specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chuntharapai A,
                                                                                                                                                                                                                              ADG98744 standard; protein; 74 AA.
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                                                                                                                                                                                                                                                                                              Apo-3/DR3 death domain protein
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98US-0074119P.
98US-00079029.
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                                                                                                                                                      ERMGLDGCVEDLRS 74
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                                                      Query Match
Best Local Similarity 100...
Ref. Conservative
                                                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity
74; Conserve
                                                                                                                                                                                                                                                                                                                                cancer; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                        US2003148455-A1
                                            Sequence 74 AA;
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09-FEB-1998;
14-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides novel Apo-2 polypeptide and the encoding polynucleotide capable of modulating apoptosis. The invention is useful in diagnosing, treating and preventing cancer, tissue typing, in generating antibodies and transgenic animals. The invention is also useful in gene therapy. The present sequence is human Apo-3/DR3 protein. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Apo-2 polypeptides and encoding nucleic acid molecules, useful for diagnosing, preventing or treating cancer, and in tissue typing or in generating antibodies or transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.3%; Score 381; DB 8; Length 74
100.0%; Pred. No. 5e-41;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim KJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chuntharapai A,
ADO40453 standard; protein; 74 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW93610 standard; protein; 65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 2B; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 97US-0046615P.
; 98US-0074119P.
; 2001US-00052798.
; 2002US-00288917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-2003; 2003US-00423448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams CW, Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERMGLDGCVEDLRS
                                                                                                                                                                    Human Apo-3/DR3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERMGLDGCVEDLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW93610;
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Gaps

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1 VMDAVPARRWKEFVRTLGLREAEIEAVEVGIGRFRDQQYEMLKRWRQQQPAGLGAVYAAL 60

Conservative

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osteoprotegerin; DR3
                                                                                                                                                                                                                                                           WPI; 2000-594575/56.
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                                                                                                                                                                                                                                      Ni J, Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 65 AA;
                                                                                                             WO200056862-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 VEDLR
                                                                                                                                                                              24-MAR-1999;
                                                                                        Homo sapiens
                                                                                                                                                                                         14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-2002
                                                                                                                                  8-SEP-2000
                                                                                                                                                                                                                                                                                                                   and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Si
Matches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG31493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG31493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ଚ
                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel human adriamycin-inducible killer protein located on chromosome 8p21, which also has p53-inducible, apoptosis-mediating activity and comprises an amino-terminal extracellular receptor, transmembrane and death domains. The nucleic acid molecule which encodes the protein, it's encoded signal transduction protein and antibodies of the invention are useful in the diagnosis and treatment of neoplastic diseases. The invention is also useful for the
                                                                                                                                                                                                                                                                                                                                       A new nucleic acid encodes a p53-induced protein (Killer) - which induces apoptosis and is useful in the diagnosis and treatment of neoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                    Killer protein; adriamycin inducible; human; chromosome 8p21; diagnosis;
p53-inducible; apoptosis-mediating activity; treatment; animal model;
neoplastic disease; DR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; tumour necrosis factor; TNF; TR9 receptor; immunosuppressive;
antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic;
antiathritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RWKEFVRTLGLREAEI EAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.8%; Score 338; DB 2; Length 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 1.5e-35; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 46; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     production of animal model systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB26990 standard; protein; 65 AA.
                                                                                                                                                                                                   97US-0054710P.
97US-0060473P.
                                                                                                                                                                                                                         98US-0077526P.
98US-0077628P.
                                                                                                                                                                   98WO-US014495
                                                                                                                                                                                         97US-0052305P
                                                                                                                                                                                                                                                98US-0077661P
                                Human DR3 protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                     (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human DR3 death domain.
                                                                                                                                                                                                                                                                                                                  WPI; 1999-120857/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEDLR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEDLR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 65 AA;
                                                                                                  Homo sapiens
                                                                                                                        WO9902653-A1
                                                                                                                                                                   10-JUL-1998;
                                                                                                                                             21-JAN-1999
                                                                                                                                                                                                                         11-MAR-1998
                                                                                                                                                                                                                                                                                          El-Deiry WS
                                                                                                                                                                                                   04-AUG-1997
                                                                                                                                                                                                             30-SEP-1997
                                                                                                                                                                                                                                                11-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                              diseases
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ID AAB2
XX
AC AAB2
XX
DT 02-F
XX
DE Huma
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Huma
KW Huma
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The present sequence is the death domain of DR3. It was used for comparison to a domain of a novel human tumour necrosis factor receptor, designated TR9. The TR9 receptor is also known as Death Domain Containing Receptor 6. TR9 polypeptides, polymucleotides or agonists are useful for treating, preventing or diagnosing common variable immunodeficiency, X-linked agammaglobulinaemia, severe combined immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such as rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis, diabetes mellitus and asthmal, HIV infection, epilepsy, cancer, cardiovascular diseases and other neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecule encoding a human tumor necrosis factor receptor, known as TR9, useful for treating, preventing and diagnosing severe combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
                                                                                                      autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis; multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer; cardiovascular disease; neurological disease; protein coordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 RWKEFVRTLGLREABIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
neuroprotective, gene therapy; Death Domain Containing Receptor common variable immunodeficiency; X-linked agammaglobulinaemia; severe combined immunodeficiency; Wiskott-Aldrich syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, Apo-2DcR, Apo-2 ligand, programmed cell death, apoptosis,
neurodegenerative disease, autoimmune, inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.8%; Score 338; DB 3; Length 65
100.0%; Pred. No. 1.5e-35;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Apo-2DcR associated protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 4C; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG31493 standard; protein; 78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0126019P.
99US-0134220P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAR-2000; 2000WO-US006831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 100. 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X S X M M X E X L X Y X L
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US2003148455-A1
                                                                                                                                                                                                                                                                                                                                                      Sequence 78 AA;
                        23-SEP-1996;
31-MAR-1997;
                                                                               Ashkenazi AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LS-MAY-1997;
             01-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG98745;
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG98745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides, designated App-2DCR, and the polymucleotide sequences encoding them. App-2DCR is capable of binding App-2 ligand and is useful for modulating programmed cell death or apoptosis in mammalian cells. App-2DCR can be used to produce app-2DCR antibodies which are useful therapeutically, and can cross-react with other receptors for App-2 ligand to block excessive apoptosis in neurodegenerative diseases, or to block potentially autoimmune or inflammatory effects. App-2DCR antibodies are also useful in immunohistochemistry staining assays or diagnostic assays for App-2DCR, e.g. detecting it's expression in specific cells, tissues or serum, and for the affinity purification of App-2DCR from recombinant cell culture or natural sources. The present sequence represents a protein of unknown function relating to the present invention. Note: The present sequence is given in the Seq listing but is not mentioned elsewhere in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated Apo-2DcR polypeptide useful for modulating apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Gaps
                                                                                                                                                                                                                                              present invention relates to the isolation of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; affinity; competitive-type receptor; binding assay; cancer cell; human; TNF receptor family; hTNFRI; death domain; cytostatic.
                                                                                                                             Kim KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
37.5%; Score 155; DB 5; Length 78;
Best Local Similarity 46.1%; Pred. No. 7e-12;
Matches 35; Conservative 13; Mismatches 24; Indels
                                                                                                                            Chuntharapai A, Gurney A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Death domain of human TNFR1 (hTNFR1) protein.
                                                                                                                                                                                                                       Disclosure; Page 37; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA49709 standard; protein; 78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAR-2002; 2002US-00112793.
                                             21-JUN-2001; 2001US-00887879
                                                                  97US-0049911P
                                                                             98US-00096500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 YAALERMGLDGCVEDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GRVLRDMDLLGCLEDI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                            Ashkenazi AJ, Baker KP,
                                                                                                   (GETH ) GENENTECH INC
                                                                                                                                                              WPI; 2002-697823/75.
                                                                                                                                                                                                mammalian cells.
US2002102706-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002192729-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 78 AA;
                                                                  18-JUN-1997;
                                                                             12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-NOV-2003
                     01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA49709;
                                                                                                                                       Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
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The present invention relates to the isolation of a biologically active Apo-2 ligand inhibitor (Apo-2LI) or Apo-3, and the polynucleotide sequences encoding them. Apo-2LI and Apo-3 are involved in apoptosis. The Apo-2LI and Apo-1 peptides are useful in diagnostic assays. Apo-2LI is useful for generating antibodies, as standards in assays for Apo-3 or Apo-2LI in affinity purification techniques, and in competitive-type receptor binding assays when labelled with radioiodine, enzymes or fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or inducing apoptosis in cancer cells, and thus have therapeutic utility. The present sequence represents the death domain of a human TNF receptor family protein. This sequence is compared with the death domain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ñ
                                                                                                                                                                                                                                                                                                                                                Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or
Apo-3 polypeptide which induces or stimulates apoptotic activity, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apo-2; apoptosis; diagnosis; tissue-specific typing; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.5%; Score 155; DB 6; Length 78; 46.1%; Pred. No. 7e-12; tive 13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADG98745 standard; protein; 78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 6; 53pp; English
                                96US-00710802.
97US-00828683.
96US-00625328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2002; 2002US-00288917.
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14-MAY-1998; 98US-00079029.
02-NOV-2001; 2001US-00052798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0046615P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 YAALERMGLDGCVEDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GRVLRDMDLLGCLEDI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3/.3%;
Best Local Similarity 46.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFR1 death domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Conservative
                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                     in diagnostic assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                              WPI; 2003-657226/62.
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5

Gaps

4,

8; Length 78; 24; Indels

37.5%; Score 155; DB 8; 46.1%; Pred. No. 7e-12; tive 13; Mismatches 2

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in diagnosing, treating and preventing cancer, tissue typing, in generating antibodies and transgenic animals. The invention is also useful in gene therapy. The present sequence is human INFR1 protein. This sequence is used in the exemplification of the invention
 polynucleotide capable of modulating apoptosis. The invention is useful
                                                                             Sequence 78 AA;
                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                  AAW93612
 8888888
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                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                       1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP----AGLGAV 56
                                                                                                                                                                                                                                                                                  The present invention provides novel Apo-2 protein and the nucleic acid encoding the protein. The invention is useful in inducing apoptosis in mammalian cancer cells. The invention is also useful in diagnostic procedures for tissue-specific typing and in generating transgenic animals that are useful in development and screening of reagents. The invention is also useful in gene therapy. The present sequence is TNPRI (tumour necrosis factor receptor 1) death domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides novel Apo-2 polypeptide and the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                  Gaps
                                          New Apo-2 polypeptide or its extracellular or death domain sequence, useful for modulating apoptosis in mammalian cancer cells or for generating transgenic or knockout animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 protein, apoptosis; cancer; tissue typing; transgenic animal;
therapy; human; TNFR1; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Apo-2 polypeptides and encoding nucleic acid molecules, useful diagnosing, preventing or treating cancer, and in tissue typing or
                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                         37.5%; Score 155; DB 7; Length 78;
46.1%; Pred. No. 7e-12;
ive 13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim
 Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          generating antibodies or transgenic animals.
Chuntharapai A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chuntharapai A,
                                                                                      Disclosure; Fig 2B; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                               ADO40454 standard; protein; 78 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 2B; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-FEB-1998; 98US-0074119P.
14-MAY-1998; 98US-00079029.
02-NOV-2001; 2001US-00052798.
06-NOV-2002; 2002US-00288917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-APR-2003; 2003US-00423448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0046615P
                                                                                                                                                                                                                                                                                                                                       76
                                                                                                                                                                                                                                                                                                                 57 YAALERMGLDGCVEDL 72
                                                                                                                                                                                                                                                                                                                                GRVLRDMDLLGCLEDI
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams CW, Ashkenazi AJ,
Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-090468/09.
                      WPI; 2003-897574/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TNFR1 protein
                                                                                                                                                                                                                                  Local Similarity
nes 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS2004009552-A1
                                                                                                                                                                                                     Sequence 78 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L5-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-2004
 Adams CW,
                                                                                                                                                                                                                                                                                                                                                                                                                     ADO40454;
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apo-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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protein located on chromosome 8p21, which also has p53-inducible, apoptosis-meditaring activity and comprises an amino-terminal extracellular receptor, transmembrane and death domains. The nucleic acid molecule which encodes the protein, it's encoded signal transduction protein and antibodies of the invention are useful in the diagnosis and treatment of neoplastic diseases. The invention is also useful for the production of animal model systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A new nucleic acid encodes a p53-induced protein (Killer) - which induces apoptosis and is useful in the diagnosis and treatment of neoplastic
                                 1 VVENVPPLRWKEFVRRLGLSDHEIDRLELQNGRCLREAQYSMLATWRRRTPRREATLELL 60
1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Killer protein, adriamycin inducible, human; chromosome 8p21; diagnosis;
p53-inducible; apoptosis-mediating activity; treatment; animal model;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel human adriamycin-inducible killer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 46; 65pp; English.
                                                                                                                                                                                                                                                                                                                           Ä
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97US-0054710P.
97US-0060473P.
98US-0077526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TNFR-1 protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US014495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0077661P
                                                                                                                   72
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                                                                                                                                                                         GRVĽRDMDĽĽĠČĽÉĎI 76
                                                                                                                                                                                                                                                                                                                        AAW93612 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neoplastic disease; TNFR-1
                                                                                                                   57 YAALERMGLDGCVEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PENNSYLVANIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYPE-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9902653-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                 AAW93612;
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GAVYAALERMGLDGCVEDLRSRLQRGP 30

(first entry)

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AAB26989 standard; protein; 68 AA
                                                                                                                                     Human TNFR 1 death domain.
                                                                                                             02-FEB-2001
                                                                                       AAB26989;
                                     RESULT 12
AAB26989
                                                               ò
                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to prytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, mematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or resamment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodilatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                9 RWKEFVRTLGLREAEIBAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAVYAALERMG 64
                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 22587; 1399pp + Sequence Listing; English.
34.4%; Score 142; DB 2; Length 69; 47.1%; Pred. No. 2.8e-10; ive 11; Mismatches 21; Indels
                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 22587.
                                                                                                                                                                                  AA008695 standard; protein; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2000; 2000US-00515126
                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-2000; 2000US-00577409
                                                                                                                                                                                                                                06-NOV-2001 (first entry)
                         32; Conservative
                                                                                                             | ||:||:
LLGCLEDI 68
                                                                                                LDGCVEDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-514838/56.
            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAI88626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                   WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-2001
                                                                                                65
                                                                                                                                                                                                           AA008695;
Query Match
                        Matches
                                                                                                                                                           RESULT 11
AAO08695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecule encoding a human tumor necrosis factor receptor, known as TR9, useful for treating, preventing and diagnosing severe combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
Human; tumour necrosis factor; TNF; TR9 receptor; immunosuppressive; antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic; antiathritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic; neuroprotective; gene therapy; Death Domain Containing Receptor 6; common variable immunodeficiency; X-linked agammaglobulinaemia; severe combined immunodeficiency; Wiskott-Aldrich syndrome; autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis; multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer; cardiovascular disease; neurological disease; protein coordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQ--OQPAGLGAVYAALERMGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4C; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fan P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAR-2000; 2000WO-US006831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0134220P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 46.3*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ບັ
                                                                                                                                                                                                                                                                                                osteoprotegerin; TNFR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ni J, Gentz RL, Yu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-594575/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 68 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200056862-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and cancer.
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Gaps

; 0

33.7%; Score 139; DB 4; Length 30; 100.0%; Pred. No. 2.5e-10; Live 0; Mismatches 0; Indels

54 GAVYAALERMGLDGCVEDLRSRLQRGP 80

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Conservative

ADG42594 standard; protein; 75 AA.

(first entry)

26-FEB-2004

ADG42594;

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RESULT 14
                   ADG42594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW00207 shows the death domain of the p55 tumour necrosis factor receptor (p55 TNF-R). The death domain (DD) of human Fas-ligand receptor (FAS-R), ankyrin 1, nerve growth factor receptor (NGF-R) and MORT-1 (which binds to the intracellular portion of (FAS-R)) are also given (see AAW00206-07 and AAW00209-W00210). These DDs are used to identify compounds capable of modulating activity of the regulatory proteins (p55, NGF, TNF and FAS-R ligand, MORT-1) vai interaction with the DDs. Such modulators which may be antibodies, antisense sequences or ribozymes (which can affect the cellular mRNA sequences encoding the proteins) and care useful for modulation of effects of the regulatory proteins and the cell. Tumour cells, HIV-infected cells or other diseased cells can be treated by targeting the cells with animal viral vectors encoding the modulators and a viral surface antigen capable of binding to a specific receptor. The DDs are characterised by having groups of common maino acid residues Trp, Ala, Asp, Glu, Thr, Arg and Tyr within locations that can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulator of regulatory cellular events mediated by "death domain" contragulatory proteins - useful for modulating functions mediated in cells by proteins contg the death domain.
                                                                                                                                                                                               Death domain; regulatory protein; NGF-R; nerve growth receptor; FAS-R; Fas ligand receptor; Fas/APO1; ankyrin 1; D55 TNF-R; tumour necrosis factor receptor; MORT1; cell cytoxicity; HIV; human immunodeficiency virus; cancer; neoplasia; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 WKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQOPAGLGAVYAALERMG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.6%; Score 118; DB 2; Length 64;
42.6%; Pred. No. 3.2e-07;
ive 10; Mismatches 17; Indels 12; Gaps
                                                                                                                                                              Human p55 tumour necrosis factor receptor death domain motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mett I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pancer Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Varfolomeev EE,
                                                  AAW00208 standard; peptide; 64 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (YEDA ) YEDA RES & DEV CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                               95IL-00112742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95IL-00115289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 42.6%
Matches 29; Conservative
                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boldin MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WEIN/) WEINWURZEL H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-402125/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 64 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soncharov TM;
                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                 WO9625941-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-1995;
                                                                                                                         16-APR-1997
                                                                                                                                                                                                                                                                                                                                                                    29-AUG-1996.
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                                                                                     AAW00208;
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1 WKEFVRRIGLSDHEIDRLELQNGRCLREAQYSMLATWRRRTPRR----EATLELLGRVLR 56

--- LDGCV 69 DHDLLGCL 64

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LLDDPLGRDWRRLARKLGLSEEEDQIEHENPRLASPTYQLLDIWEQRGGKNATVGTLLE 65
                                                                                            cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical; NOVX-associated disorder; cancer; NOVX; domain analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                         New NOVX gene or NOVX-specific antibody, useful for preparing a composition for treating or preventing a NOVX-associated disorder, e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQ--QPAGLGAVYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Indels
                                                                NOV1 domain analysis associated protein seq id 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.4%; Score 105; DB 7; 35.3%; Pred. No. 1.8e-05; iive 12; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 47; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                          Shimkets RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADO40451 standard; protein; 76 AA.
                                                                                                                                                                                                                                            04-OCT-2001; 2001US-00970944.
                                                                                                                                                                                                                                                                            04-OCT-2000; 2000US-0237862P.
                                                                                                                                                                                                                                                                                                                                                                          Herrmann JL, Rastelli L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Apo-2 protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in human NOV1 protein.
                                                                                                                                                                                                                                                                                                        (HERR/) HERRMANN J L.
(RAST/) RASTELLI L.
(SHIM/) SHIMKETS R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 ALERMGLD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALRKWGRD 73
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-900673/82.
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                                                                                                                                                                             JS2003204052-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 75 AA;
                                                                                                                                               Jnidentified.
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                                                                                                                                                                                                            30-OCT-2003.
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Best Local S
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Length 76; 19; 29; Indels

Query Match 22.8%; Score 94; DB 8; I Best Local Similarity 34.4%; Pred. No. 0.00049; Matches 22; Conservative 11; Mismatches 29,

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61 ERMG 64 | :| 63 ETLG 66

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Search completed: June 27, 2005, 14:37:58 Job time : 160 secs

3 DAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQOYEMLKRW--RQQOPAGLGAVYAAL

Sequence 23, Ag Sequence 23, A Sequence 23, A

Sequence 3, Appli Sequence 26, Appli Sequence 26, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 25, Appli Sequence 22, Appli Sequence 118, Appli Sequence 21, Appli Sequence 21, Appli Sequence 721, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 11, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli

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1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAAL
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                                                                                                                                                                                                                                                            US-10-041-574-25
US-10-041-574-25
US-10-014-254-56
US-10-424-599-188281
US-10-656-250-118
US-10-035-408-1
US-09-756-692-721
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US-10-001-254-53
                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-041-574-22
US-10-040-862-721
US-10-057-475B-721
US-10-154-884B-721
US-10-764-324-721
US-10-834-966-22
                   US-09-756-854-23

US-10-041-574-23

US-10-035-408-3

US-10-035-408-3

US-10-035-408-3

US-10-041-574-26

US-10-041-574-26

US-10-041-574-26

US-10-207-295-8

US-10-207-295-8

US-10-287-59-8

US-10-287-59-8
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US-09-992-964-17
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J Sequence 15, Application US/09887879
J Sequence No. US20020102706A1
GENERAL INFORMATION:
J APPLICANT: Baker, Kevin P.
APPLICANT: Chuntharapai, Anan
APPLICANT: Gurney, Austin
APPLICANT: Kim, Kyung Jin
APPLICANT: Kim, Kyung Jin
APPLICANT: Wood, William I.
J TILLE OF INVENTION: Apo-2DCR
FILE REFERENCE: P1110P1
CURRENT APPLICATION NUMBER: US/09/887,879
CURRENT PILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 17
LENGTH: 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
RESULT 1
US-09-887-879-15
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Sequence 15, Appl
Sequence 15, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 23, Appl
Sequence 10, Appl
                                                                                                                                 June 27, 2005, 14:38:10 ; Search time 163 Seconds (without alignments) 188.735 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

1: /cgn2 6/ptodata/1/pubpaa/USO7 PUBCOWB.pep:*
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-922-964-15

US-10-207-295-9

US-10-242-383-15

US-09-756-854-24

US-10-084-24

US-10-084-966-24

US-09-887-879-16

US-09-982-964-16

US-09-922-964-16

US-10-112-793-23

US-10-207-295-10
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                                                                                                                                                                                                                                                                                                                                                                      1717557 seqs, 384547976 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   protein search, using sw model
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Match Length
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Perfect score:
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ALIGNMENTS

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PRIOR APPLICATION DATA:
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-756-854-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 92.3%; Score 381; DB 9; Length 74 Best Local Similarity 100.0%; Pred. No. 1.2e-38; Matches 74; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                         APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin
APPLICANT: Baker, Kevin
APPLICANT: Gurney, Austin
APPLICANT: Wood, William
ITILE OF INVENTION: Apo-2DCR
FILE REFERENCE: P1110
CURRENT APPLICATION NUMBER: U8/09/992,964
CURRENT APPLICATION NUMBER: 08/678,168
PRIOR FILING DATE: 1997-06-18
NUMBER: OF SEQ ID NOS: 17
LENGTH: 74
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Sequence 9, Application US/10207295

Publication No. US20030017161A1

GENERAL INFORMATION:

APPLICANT: Ankenazi, Avi J.

APPLICANT: Chuntharapai, Anan

APPLICANT: Kim, Kyung Jin

TILE OB INVENTION: AP0-2 RECEPTOR

FILE REFERENCE: 11669.28US04

CURRENT APPLICATION NUMBER: US/10/207.295

CURRENT FILING DATE: 2002-07-29

PRIOR PELLOR DATE: 1998-02-09

PRIOR FILING DATE: 1998-02-09

PRIOR FILING DATE: 1997-05-15

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PARCENTIN VET: 2.00

SEQ ID NO 9

LENGTH: 74
                                                                                                                 US-09-992-964-15
Sequence 15, Application US/09922964
Facent No. US20020161202A1
GENERAL INFORMATION:
                       ERMGLDGCVEDLRS 74
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Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-09-992-964-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VMDAVPARRWKEFVRTLGLREAEIEAVEVBIGRFRDQQYEMLKRWRQQQPAGLGAVYAAL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ni, Jian
Yu, Guo-Liang
Pan, Ping
Gent, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 74;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
92.3%; Score 381; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.2e-38;
Matches 74; Conservative 0; Mismatches 0;
                                                                                                                   APPLICANT: Baker, Kevin P.
APPLICANT: Chuntharapai, Anan
APPLICANT: Curney, Austin
APPLICANT: Kim, Kyung Jin
APPLICANT: Wood, William I.
TITLE OF INVENTION: Apo-2DCR
FILE REFERENCE: P1110P1
CURRENT APPLICATION NUMBER: US/10/242,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,854
FILING DATE: 10-3an-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US/10/242,383

PRIOR APPLICATION NUMBER: US/09/887,879

PRIOR FILING DATE: 2001-06-21

PRIOR APPLICATION NUMBER: 09/096,500

PRIOR PILING DATE: 1998-06-12

PRIOR PLING DATE: 1998-06-12

PRIOR PILING DATE: 1997-06-18

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 15

LENGTH: 74
US-10-242-383-15; Sequence 15, Application US/10242383; Publication No. US20030138915A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 24, Application US/09756854; Patent No. US20020164684A1; GENERAL INFORMATION:
                                                                                                   APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ERMGLDGCVEDLRS 74
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APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
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CORGANISM: Homo sapiens
US-10-834-966-24
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ORGANISM: Homo sapiens
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                                                                                                                                                            GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/10041574
Publication No. US20020168359A1
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Fan, Ping
APPLICANT: Fan, Ping
APPLICANT: Fan, Ping
APPLICANT: Fan, Fang
FILE REFERENCE: PF375P1
FILE REFERENCE: PF375P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
81.8%; Score 338; DB 9; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 65; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: F43.75FL
CURRENT PELLOXION NUMBER: US/10/041,574
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: 09/527,236
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2900-03-16
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-10
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 27
SEQ ID NOS: 27
SEQ ID NOS: 27
SEQ ID NOS: 27
                                                          NAME: HOOVET, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF375
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
TYPE: SEGNENESS: single
                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-756-854-24
APPLICATION NUMBER: 09/095,094
                      FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-10-041-574-24
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CLASSIFICATION: <Unknown>
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LENGTH: 78
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                                                                                                                                         1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAV 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.5%; Score 155; DB 9; Length 78; llarity 46.1%; Pred. No. 5e-11; Conservative 13; Mismatches 24; Indels
                                    37.5%; Score 155; DB 9; Length 78;
46.1%; Pred. No. 5e-11;
tive 13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/10112793
; Sequence 23, Application US/2012019272941
; Publication No. US2002019272941
; Publication No. US2002019272941
; Publication No. US2002019272941
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA WAY
; CITY: South San Francisco
; STRTE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/09992964
; Betten No. US20020161202A1
; GENERAL INFORMATION:
; APPLICANT: Abikenazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Baker, Kevin
; APPLICANT: Gurney, Austin
; APPLICANT: Wood, William
; TILE OF INVENTION: Apo-2DCR
; FILE REFERENCE: P1110
CURRENT APPLICATION NUMBER: US/09/992,964
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 08/878,168
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 78
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APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
                                                                                                                                                                                                                        61 GRVLRDMDLLGCLEDI 76
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                                                                                                                                                                                                57 YAALERMGLDGCVEDL 72
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                                                                               Conservative
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US-09-992-964-16
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Best Local Similarity
---a 35; Conserve
                              Query Match
Best Local Similarity
Matches 35; Conserv
US-09-887-879-16
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1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDOQYEMLKRWRQOOP---AGLGAV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VVENVPPLRWKEFVRRLGLSDHEIDRLELQNGRCLREAQYSMLATWRRRTPRREATLELL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.5%; Score 155; DB 13; Length 78; 46.1%; Pred. No. 5e-11; tive 13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%; Score 155; DB 14; Length 78;
46.1%; Pred. No. 5e-11;
tive 13; Mismatches 24; Indels
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
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Sequence 10, Application US/10207295
Publication No. US20030017161A1
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
TITLE OF INVENTION: APO-2 RECEPTOR
FILE REFERENCE: 11669-28US04
CURRENT APPLICATION NUMBER: US/10/207,295
CURRENT FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US/09/020,746
PRIOR APPLICATION NUMBER: 08/857,216
PRIOR FILING DATE: 1997-05-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                      FILING DATE: 23-Sep-1996
ATTORNEY/AGRNT INFORMATION:
NAME: Marschang, Diane L.
ROSTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                 FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-495
APPLICATION NUMBER: 08/710802
                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 78 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GRVLRDMDLLGCLEDI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 YAALERMGLDGCVEDL 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 46.1
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 46.1
Matches 35; Conservative
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Gaps

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1 RWKEFVRRIGLSDHEIDRLELQNGRCLREAQYSMLATWRRTRREATLELLGRVLRDMDL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 RWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQ--QQPAGLGAVYAALERMGL
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APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Fan, Ding
APPLICANT: Fan, Ping
APPLICANT: Fan, Ping
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375P1
CURRENT APPLICATION NUMBER: US/10/041,574
CURRENT FILING DATE: 2002-01-10
PRIOR PRIOR APPLICATION NUMBER: 09/527,236
PRIOR APPLICATION NUMBER: 09/527,236
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-03-24
PRIOR FILING DATE: 1999-03-24
PRIOR FILING DATE: 1999-03-14
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.1%; Score 136.5; DB 13; Length 68; 46.3%; Pred. No. 7.7e-09; tive 12; Mismatches 21; Indels 3
                                                                                                                                                                                                                                                                                                                                                       Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                     21; Indels
                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                  33.1%; Score 136.5; DB 9 46.3%; Pred. No. 7.7e-09; tive 12; Mismatches 21
                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-756-854-23
REGISTRATION NUMBER: 40,302
                        REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/10041574 Publication No. US20020168359A1 GENERAL INFORMATION:
                                                                 TELEPHONE: 301-309-8504
                                                                                       TELEPAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 46.38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 46.3*
Matches 31; Conservative
                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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61 LGCLEDI 67
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61 LGCLEDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fan, Ping
Gentz, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.5%; Score 155; DB 14; Length 78;
46.1%; Pred. No. 5e-11;
tive 13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/756,854
FILING DATE: 10-Jan-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                             HUBICATION OF USZUGJOISFISAL

APPLICANT: Aahkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
APPLICANT: Curney, Austin
APPLICANT: Gurney, Austin
APPLICANT: Kim, Kyung Jin
APPLICANT: Wood, William I.
TITLE OF INVENTION: Apo-2DCR
FILE REFREENCE: PILIOPI
CURRENT APPLICATION NUMBER: US/09/887, 879
FRIOR FILING DATE: 2002-06-12
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

**APPLICATION NUMBER: 09/095,094

**PILING DATE: 
    ATTORNEY/AGENT INFORMATION:

                 5-10-242-383-16
Sequence 16, Application US/10242383
Publication No. US20030138915A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23, Application US/09756854 Patent No. US20020164684A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hoover, Kenley K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ni, Jian
Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | | ||:||:
61 GRVLRDMDLLGCLEDI 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 46.1
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-242-383-16
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65 9

Gaps

Search completed: June 27, 2005, 14:53:23 Job time : 164 secs

66 DGCVEDL 72 ||:||: 61 LGCLEDI 67

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24, Appl 27, Appl 4, Appl 4, Appl 5122, Ap

Appli Appli

Sequence Sequence Sequence Sequence

21, Appl 21, Appl 10142, A

Sequence Seq

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OM protein

Run on:

Searched:

Database

Result No.

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1 RWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 RWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                    NE-09-527-236A-24

Sequence 24 Application US/09527236A

Sequence 24 Application US/09527236A

Sequence 25 Application US/09527236A

SERENAL INFORMATION:

APPLICANT: Ni, Jian

APPLICANT: Yu, Guo-Liang

APPLICANT: Tu, Guo-Liang

APPLICANT: Reiner L.

ITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9

FILE REFERENCE: PR375P1

CURRENT PFLING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/052,991

PRIOR PFLING DATE: 1997-06-11

PRIOR PFLING DATE: 1999-06-14

PRIOR PLING DATE: 1999-06-14

PRIOR PLING DATE: (1999-03-24

PRIOR PLING DATE: (1999-05-14

PRIOR PLING DATE: (1999-05-14

PRIOR PLING DATE: (1999-05-14

PRIOR PLING DATE: 1999-05-14

SOFTWARE: Patentin Ver: 2.1

SOFTWARE: Patentin Ver: 2.1
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               US-09-756-854-22
US-09-159-277A-5
US-08-828-683A-24
US-08-828-628-2
US-08-894-626-2
US-08-894-626-2
US-09-134-001C-5122
US-09-134-001C-5122
US-09-134-001C-3335
US-09-134-001C-3335
US-09-134-001C-3898
US-09-134-001C-3898
US-09-134-001C-3898
US-09-134-001C-3898
US-09-134-001C-3898
US-09-134-001C-3898
US-09-134-001C-3898
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Patent No. 6667390
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
Fan, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 100.
65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEDLR 65
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 US-09-527-236A-24
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Query Match
Best Local S
Matches 65
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Sequence 23, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 26, Appl
Thence 27, Appl
Thence 22, Appl
Thence 23, Appl
Thence 24, Appl
Thence 25, Appl
Thence 26, Appl
Thence 26, Appl
Thence 27, Appl
Thence 27, Appl
Thence 27, Appl
Thence 26, Appl
Thence 27, App
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Sequence 1, Appli
                                                                                                                                           (without alignments)
138.882 Million cell updates/sec
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Sequence 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                       1 VMDAVPARRWKEFVRTLGLR......ERMGLDGCVEDLRSRLQRGP
                                                                                                                            June 27, 2005, 14:32:34 ; Search time 43 Seconds
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'/ Cgn2 of ptodata1/liaa/5A_COMB.pep:*
'/ Cgn2 of ptodata1/liaa/5B_COMB.pep:*
'/ Cgn2 of ptodata1/liaa/6A_COMB.pep:*
'/ Cgn2 of ptodata1/liaa/6B_COMB.pep:*
'/ Cgn2 of ptodata1/liaa/BCMS.pep:*
'/ Cgn2 of ptodata1/liaa/PCTUS CCMB.pep:*
'/ Cgn2 of ptodata1/liaa/PCTUS CCMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-995-050-1
US-08-219-237B-10
US-08-894-626-1
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                                                                                                                                                                                                                                                                                                                               513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                     US-10-081-280-6_COPY_338_417
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Maximum Match 100%
Listing first 45 summaries
                                                                                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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16.5
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16.2
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Sequence:
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338
155
142
142
136.5
136.5
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57.5
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NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442107001
TELECOMUNICATION INFORMATION:
TELEPHONE: (650)813-5600
                                                                                                                                                                                                                                                                                                                                                            LENGTH: 78 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                               TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 YAALERMGLDGCVEDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | | ||:||:
61 GRVLRDMDLLGCLEDI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-828-683A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
               TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9 NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPSY disk

MEDIUM TYPE: RIOPSY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/756,854

FILING DATE: 10-Jan-2001

CLASSIFICATION: -UNKNOWN>
PRIOR APPLICATION NUMBER: 09/095,094

FILING DATE: -CURROWN>
APPLICATION NUMBER: 09/095,094

ATTORNEY/AGENT INFORMATION:

NAME: HOOVEY, Kenley K.

REGISTRATION NUMBER: 40,302

REFERENCE/DOCKET NUMBER: PF375

TELEPHONE: 300-98504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

81.8%; Score 338; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 6.2e-37;
Matches 65; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STREE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-756-854-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/08828683A Patent No. 6469144 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 65 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
Sentz, Reiner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                        CITY: Rockville
                                                                                                                                                                  COUNTRY: US
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1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAV 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09159277A
| Batent No. 6562797
| GENERAL INPOMATION:
| APPLICANT: DIXIT, VISHVA M. APPLICANT: O'ROURKE, KAREN
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING TITLE OF INVENTION: PSA-ASSOCIATED APOPTOSIS
| NUMBER OF SEQUENCES: 10
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.5%; Score 155; DB 4; Length 78; 46.1%; Pred. No. 7.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,277A
                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1966
APPLICATION NUMBER: 08/710802
FILING DATE: 23-589-196
ATORNEY AGENT INFORMATION:
NAME: MATECHANG, DIANE L.
REGISTRATION NUMBER: 35,600
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 65/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.1%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/844,691
PILING DATE: 21-APR-1997
APPLICATION UNDERER: US 08/416,379
FILING DATE: 03-APR-1995
ATTORNEY/AGENT INFORMATION:
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755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
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JS-09-527-236A-23
                          NAME/KEY:
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        FEATURE:
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Matches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                         4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08844691A
Patent No. 6747138
Patent No. 6747138
GENERAL INFORMATION:
APPLICANT: DIXIT, VISHVA M.
APPLICANT: O'ROURKE, KAREN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING
TITLE OF INVENTION: FAS-ASSOCIATED APOPTOSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTTISON & FOOTSTELLP
                                                                                                                                                                                                                                                                                                                                           Query Match 34.4%; Score 142; DB 4; Length 70; Best Local Similarity 47.1%; Pred. No. 3.4e-11; Matches 32; Conservative 11; Mismatches 21; Indels
                                                                                                                                                                                                                                   LOCATION: 11

OTHER INFORMATION: /note= "Leu is replaced by Asn for OTHER INFORMATION: the point mutant hTNFR-1"
US-09-159-277A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Proppy disk
COMPUTER: PROPPY disk
COMPUTER: PROPPICATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,691A
FILING DATE: 21-APR-1997
CLASSIFICATION: 536
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APPLICATION DATA:
APPLICATION NUMBER: US 08/416,379
FILING DATE: 03-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: KORBKÍ, ANTOINETE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442107001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
TELEPAX: (650)494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (650)494-0792
TELEX: 706141 MRSNFOBRS SFO
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 NAME/KEY: Modified-site
                                                                                        70 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 amino acids
                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ||:||:
61 LLGCLEDI 68
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                                                                                      LENGTH:
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1 RWKEFVRRLGLSDHEIDRLELQNGRCLREAQYSMLATWRRTFPREATLELLGRVLRDMD 60
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Gentz, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | JAPELICANT: Ni, Jian |
| APPLICANT: Ni, Jian |
| APPLICANT: Fan, Ping |
| APPLICANT: Fan, Ping |
| APPLICANT: Fan, Ping |
| APPLICANT: Gentz, Reiner L. |
| TILLE REFERENCE: PR375P1 |
| CURRENT APPLICATION NUMBER: US/09/527,236A |
| CURRENT FILING: DATE: 2000-03-16 |
| PRIOR PILICATION NUMBER: 60/052,991 |
| PRIOR PILING DATE: 1997-06-11 |
| PRIOR PILING DATE: 1998-06-10 |
| PRIOR FILING DATE: 1998-06-10 |
| PRIOR FILING DATE: 1998-05-14 |
| PRIOR FILING DATE: 1999-03-24 |
| PRIOR PLEATION NUMBER: 60/134,220 |
| PRIOR PLEATION NUMBER: 60/134,220 |
| PRIOR PLEATION DATE: 1999-03-24 |
| PRIOR PLEATION DATE: 1990-03-24 |
| PRIOR PLEATION DATE: 1990-0
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                                                                                                                                                                                                                                                                          / Match 34.4%; Score 142; DB 4; Length 70; Local Similarity 47.1%; Pred. No. 3.4e-11; nes 32; Conservative 11; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                               /note= "Leu is replaced by Asn for
the point mutant hTNFR-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/09527236A Patent No. 6358508 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 23, Application US/09756854; Patent No. 6667390; GENERAL INFORMATION:
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Yu, Guo-Liang
Modified-site
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ORGANISM: Homo sapiens
US-09-527-236A-23
                                       LOCATION: 11
CTHER INFORMATION:
CTHER INFORMATION:
US-08-844-691A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ||:||:
61 LLGCLEDI 68
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61 LGCLEDI 67
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.1%; Score 136.5; DB 4; Length 68; 46.3%; Pred. No. 1.7e-10; tive 12; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METT, Igor
GONCHAROV, Tanya M.
WEITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: MD
                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,854
FILING DATE: 10-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF375
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/095,094
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: HOOVER, KENLEY K.
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08894626
Patent No. 6355780
GENERAL INFORMATION:
APPLICANT: WALLACH, David
BOLDIN, MARK P.
VARFOLOMEEV, Eugene E.
PANCER, Zeev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                   ZIP: 20850
COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 46.3%
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C.
COUNTRY: USA
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||:||:
61 LGCLEDI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 DGCVEDL 72
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10 WKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQPAGLGAVYAALERMG----
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Patent No. 5874546
GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: TOW, Noto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: James W. Hellwege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.6%; Score 118; DB 3; Length 64; 42.6%; Pred. No. 4.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Mismatches 17; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                  CURRENT APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US/08/894,626
FILING DATE: 09-Dec-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 112,742
FILING DATE: 22-REB-1995
APPLICATION NUMBER: IL 115,289
FILING DATE: 13-SEP-1995
APPLICATION NUMBER: PCT/US96/02326
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REFERENCE/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
TELEPHONE: (202) 1777-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECILE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-894-626-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 64 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 ---LDGCV 69
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STRANDEDNESS: single
                                                                     ZIP: 20850
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Zzb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-444-005-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 WEPLMRKIGLMDNEIKVAKAEAAGHRDTLYTMLIKWVNKTGRDASVHTLLDALETIG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Gentz, Reiner
IITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCE: 26
CORRESPONDENCE ADDRESS:
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APPLICANT: Ni, Jan
APPLICANT: Yi, Guo-Liang
APPLICANT: Yi, Guo-Liang
APPLICANT: Fan, Ping
APPLICANT: Fan, Ping
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375P1
CURRENT APPLICATION NUMBER: US/09/527,236A
CURRENT APPLICATION NUMBER: 60/052,991
PRIOR FILING DATE: 1997-06-11
PRIOR PILING DATE: 1997-06-10
PRIOR PLING DATE: 1998-06-10
PRIOR PLING DATE: 1999-06-10
PRIOR PLING DATE: 1999-06-10
PRIOR PLING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: 60/126,019
PRIOR PELING DATE: 1999-05-14
PRIOR PELING DATE: 1999-05-14
SPRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTHE FALLOR FAL
                                                                                                                                                                                                                                                                                                                                                                                                Length 45;
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                                                                                                                                                                                                                                                                                                                                                                                         Score 102.5; DB 2; Length
Pred. No. 2.9e-06;
8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 KEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP 50
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STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/09527236A Patent No. 6358508 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/09756854
Patent No. 6667390
GENERAL INFORMATION:
APPLICANT: Ni, Jian
Yu, Guo-Liang
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 510
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                            24.8%;
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 51.2.
Best Local Similarity 51.2.
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Best Local Similarity 33.33
Matches 19; Conservative
                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-219-237B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-527-236A-26
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Gaps
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COMPUTER: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,854
FILING DATE: 10-Jan-2001
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/095,094
FILING DATE: «Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HOOVEY, Kenley K.
REGISTRATION NUMBER: 90,302
REGISTRATION NUMBER: 90,302
REGISTRATION NUMBER: PF375
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 20.1%; Score 83; DB 4; Length 67; Best Local Similarity 33.3%; Pred. No. 0.0018; Matches 19; Conservative 11; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Leder, Philip
APPLICANT: Seed, Brian
APPLICANT: Stanger, Ben Z.
APPLICANT: Stanger, Ben Z.
APPLICANT: Kim, Emily
TITLE OF INVENTION: CELL DEATH PROTEIN
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTATION NUMBER: 30,164
REFERENCE/POCKET NUMBER: 00383/026001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-756-854-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/08444005; Patent No. 5674734; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
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7 KHWKNCARKLGFTQSQIDEIDHDYERDGLKEKVYQMLQKWVMREGIKGATVGKLAQALHQ 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva M
TITLE OF INVENTION: RAIDD, A No. 6495322el Death Adaptor Molecule
FILE REFERENCE: 1488.0866002
CURRENT APPLICATION NUMBER: US/09/545,605
CURRENT FILING DATE: 2001-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.
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                                                                                                        Sequence 27, Application US/08828683A
Sequence 27, Application US/08828683A
Batent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 FOLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURREY APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A FLING DATE: 31-Mar-1997 CLASSIPICATION OFFER: 08/62528 FILING DATE: 1-Apr-1996 APPLICATION NUMBER: 08/625328 FILING DATE: 1-Apr-1996 APPLICATION NUMBER: 08/710802 FILING DATE: 23-Sep-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear SEQID NO: 27: US-08-828-683A-27
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PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60,033,868
PRIOR FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                     CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650/225-5416
TELEFAX: 650/525-981
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 7, Application US/09545605; Patent No. 6495322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 77 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                  STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 25.09
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                            US-08-828-683A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-545-605-7
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                                                                                                                                                                                                                                                                                                                                             Gaps
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Requent No. 6130079

GENERAL INFORMATION:
APPLICANT: DIXIT, VISHVA M.
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: RAIDD, A NOVEL DEATH ADAPTOR MOLECULE NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: MACHINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 70.5; DB 3; Length 77; 25.0%; Pred. No. 0.091; tive 19; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                              Query Match 17.8%; Score 73.5; DB 1; Length 41; Best Local Similarity 48.4%; Pred. No. 0.017; Matches 15; Conservative 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLEARATING SYSTEM: PC-DOS/NS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/995,159 FILING DATE: Herewith CLASSIFFFARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: RELUCATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,868
FILING DATE: 20-DEC-1996
CLASSIFICATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1488.086001
TELEPONINICATION INFORMATION:
TELEPONINICATION INFORMATION:
TELEPENCE (202) 371-2600
TELEPENCE (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                        21 EAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                2 EHELERDENGRCLREAGYSMLEAWRRTP 32
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DK
SOFTWARE: PALENITH PAINACE:
TELECOMMUNICATION INFORMATION:
                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: not relevant
                     TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-444-005-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity ;
                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-08-995-159-7
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                                                                             Query Match 17.1%; Score 70.5; DB 4; Length 77; Best Local Similarity 25.0%; Pred. No. 0.091; Matches 15; Conservative 19; Mismatches 21; Indels
; SEQ ID NO 7
; LENGTH: 77
; TYPE: PRT
; ORGANISM: HOMO SADIENS
US-09-545-605-7
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Search completed: June 27, 2005, 14:42:24 Job time : 44 secs

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